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(51) Int.Cl.<sup>6</sup> C12N 15/57, C12Q 1/70, C12N 15/62, C12N 9/50, C12Q 1/37

(30) 1990/04/04 (07/505,433) US

(54) **PROTEASE DU VIRUS DE L'HEPATITE C**

(54) **HEPATITIS C VIRUS PROTEASE**

(57) On identifie, on clone et on exprime la protéase nécessaire au traitement polyprotéique dans le virus de l'hépatite C. On décrit des protéases, des protéases tronquées et des protéases modifiées utiles au clivage de polypeptides spécifiques, ainsi qu'à l'analyse et à la conception d'agents antiviraux spécifiques au virus de l'hépatite C.

(57) The protease necessary for polyprotein processing in Hepatitis C virus is identified, cloned, and expressed. Proteases, truncated protease, and altered proteases are disclosed which are useful for cleavage of specific polypeptides, and for assay and design of antiviral agents specific for HCV.

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ABSTRACT OF THE DISCLOSURE

The protease necessary for polyprotein processing in Hepatitis C virus is identified, cloned, and expressed. Proteases, truncated protease, and  
5 altered proteases are disclosed which are useful for cleavage of specific polypeptides, and for assay and design of antiviral agents specific for HCV.

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**CLAIMS:**

1. A purified protease derived from the NS3 region of hepatitis C virus as shown in Figure 1 or truncations thereof having protease activity.
2. A purified protease according to claim 1 wherein said  
5 protease comprises a partial internal amino acid sequence substantially as shown in amino acids 135-145 of Figure 1.
3. A purified protease according to claim 1 or 2 wherein said protease comprises a partial internal amino acid sequence substantially as shown in amino acids 217-225 of Figure 1.
- 10 4. A purified protease derived from the NS3 region of hepatitis C virus wherein said protease comprises a partial internal amino acid sequence substantially as shown in amino acids 1-199 of Figure 1.
5. A purified protease according to claim 4 wherein said protease comprises a partial amino acid sequence substantially as shown in  
15 amino acids 1-299 of Figure 1.
6. A purified protease according to any one of the preceding claims wherein said protease comprises the amino acid sequence substantially as shown in amino acids 1-686 of Figure 1.
7. A purified protease according to any one of claims 1 to 3  
20 wherein said protease comprises a partial internal amino acid sequence substantially as shown in amino acids 60-262 of Figure 1.
8. A purified protease according to any one of the preceding claims wherein said protease comprises at least one of a histidine, aspartate and serine residue at positions corresponding to amino acids 1084, 1108 and 1166,  
25 respectively, of the hepatitis C virus polyprotein.
9. A fusion protein comprising a suitable fusion partner fused to a protease or polypeptide as defined in any one of the preceding claims.

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10. A fusion protein according to claim 9 wherein said fusion partner is selected from the group consisting of human superoxide dismutase, ubiquitin, yeast  $\alpha$ -factor, IL-2S,  $\beta$ -galactosidase,  $\beta$ -lactamase, horseradish peroxidase, glucose oxidase and urease.

5 11. A polynucleotide encoding a fusion protein comprising a protease or polypeptide as defined in any one of claims 1 to 8; and a fusion partner.

12. A polynucleotide according to claim 11 wherein said fusion partner is selected from the group consisting of human superoxide dismutase, 10 ubiquitin, yeast  $\alpha$ -factor, IL-2S,  $\beta$ -galactosidase,  $\beta$ -lactamase, horseradish peroxidase, glucose oxidase and urease.

13. An expression vector for producing an hepatitis C virus protease in a host cell, which vector comprises:

(a) a polynucleotide encoding a protease or polypeptide as defined 15 in any one of claims 1 to 8;

(b) transcriptional and translational regulatory sequences functional in said host cell, operably linked to said polynucleotide; and

(c) a selectable marker.

14. A vector according to claim 13 which further comprises a 20 sequence encoding a fusion partner, linked to said polynucleotide to form a fusion protein upon expression.

15. A vector according to claim 14 wherein said fusion partner is selected from the group consisting of human superoxide dismutase, ubiquitin, yeast  $\alpha$ -factor, IL-2S,  $\beta$ -galactosidase,  $\beta$ -lactamase, horseradish peroxidase, 25 glucose oxidase and urease.

16. A method for assaying compounds for activity against hepatitis C virus, which method comprises:

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(a) providing a protease derived from the NS3 region of hepatitis C virus;

(b) contacting said protease with a compound capable of inhibiting serine protease activity; and

5 (c) measuring inhibition of the proteolytic activity of said protease.

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HEPATITIS C VIRUS PROTEASE

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Technical Field

15 This invention relates to the molecular biology and virology of the hepatitis C virus (HCV). More specifically, this invention relates to a novel protease produced by HCV, methods of expression, recombinant protease, protease mutants, and inhibitors of HCV protease.

Background of the Invention

20 Non-A, Non-B hepatitis (NANBH) is a transmissible disease (or family of diseases) that is believed to be virally induced, and is distinguishable from other forms of virus-associated liver disease, such as those caused by hepatitis A virus (HAV), hepatitis B virus (HBV), delta hepatitis virus (HDV), cytomegalovirus (CMV) or Epstein-Barr virus (EBV). Epidemiologic evidence suggests that there may be three types of NANBH: the water-borne epidemic type; 25 the blood or needle associated type; and the sporadically occurring (community acquired) type. However, the number of causative agents is unknown. Recently, however, a new viral species, hepatitis C virus (HCV) has been identified as the primary (if not only) cause of blood-associated NANBH (BB-NANBH). See for

example, PCT WO89/046699.

Hepatitis C appears to be the major form of transfusion-associated hepatitis in a number of countries, including the United States and Japan. There is also evidence implicating HCV in induction of hepatocellular carcinoma. Thus, a need exists for an effective method for treating HCV infection: currently, there is none.

Many viruses, including adenoviruses, baculoviruses, comoviruses, picornaviruses, retroviruses, and togaviruses, rely on specific, virally-encoded proteases for processing polypeptides from their initial translated form into mature, active proteins. In the case of picornaviruses, all of the viral proteins are believed to arise from cleavage of a single polyprotein (B.D. Korant, CRC Crit Rev Biotech (1988) 8:149-57).

S. Pichuanes et al, in "Viral Proteinases As Targets For Chemotherapy" (Cold Spring Harbor Laboratory Press, 1989) pp. 215-22, disclosed expression of a viral protease found in HIV-1. The HIV protease was obtained in the form of a fusion protein, by fusing DNA encoding an HIV protease precursor to DNA encoding human superoxide dismutase (hSOD), and expressing the product in *E. coli*. Transformed cells expressed products of 36 and 10 kDa (corresponding to the hSOD-protease fusion protein and the protease alone), suggesting that the protease was expressed in a form capable of autocatalytic proteolysis.

T.J. McQuade et al, Science (1990) 247:454-56 disclosed preparation of a peptide mimic capable of specifically inhibiting the HIV-1 protease. In HIV, the protease is believed responsible for cleavage of the initial p55 gag precursor transcript into the core structural proteins (p17, p24, p8, and p7). Adding 1  $\mu$ M inhibitor to HIV-infected peripheral blood lymphocytes in culture reduced the concentration of processed HIV p24 by about 70%. Viral maturation and levels of infectious virus were reduced by the protease inhibitor.

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**Disclosure of the Invention**

We have now invented recombinant HCV protease, HCV protease fusion proteins, truncated and altered HCV proteases, cloning and expression vectors therefore, and methods for identifying antiviral agents effective for treating  
5 HCV.

According to a first aspect of the invention, there is provided a purified protease derived from the NS3 region of hepatitis C virus as shown in Figure 1 or truncations thereof having protease activity.

The protease may comprise a partial internal amino acid sequence  
10 substantially as shown in amino acids 135-145 of Figure 1, amino acids 217-225 of Figure 1, amino acids 60-262 of Figure 1 or amino acids 1-686 of Figure 1.

According to a second aspect of the invention, there is provided a purified protease derived from the NS3 region of hepatitis C virus wherein said protease comprises a partial internal amino acid sequence substantially as shown  
15 in amino acids 1-199 of Figure 1.

The protease may comprise a partial amino acid sequence substantially as shown in amino acids 1-299 of Figure 1 or amino acids 1-686 of Figure 1.

Preferably, the above-described proteases comprise at least one of  
20 a histidine, aspartate and serine residue at positions corresponding to amino acids 1084, 1108 and 1166, respectively, of the hepatitis C virus polyprotein.

According to a third aspect of the invention, there is provided a fusion protein comprising a suitable fusion partner fused to any one of the above-described proteases or polypeptides.



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Preferably, the fusion partner is selected from the group consisting of human superoxide dismutase, ubiquitin, yeast  $\alpha$ -factor, IL-2S,  $\beta$ -galactosidase,  $\beta$ -lactamase, horseradish peroxidase, glucose oxidase and urease.

According to a fourth aspect of the invention, there is provided a  
5 polynucleotide encoding a fusion protein comprising any one of the above-described proteases or polypeptides and a fusion partner.

Preferably, the fusion partner is selected from the group consisting of human superoxide dismutase, ubiquitin, yeast  $\alpha$ -factor, IL-2S,  $\beta$ -galactosidase,  $\beta$ -lactamase, horseradish peroxidase, glucose oxidase and urease.

10 According to a fifth aspect of the invention, there is provided an expression vector for producing an hepatitis C virus protease in a host cell, which vector comprises:

(a) a polynucleotide encoding any one of the above-described proteases or polypeptides;

15 (b) transcriptional and translational regulatory sequences functional in said host cell, operably linked to said polynucleotide; and

(c) a selectable marker.

Preferably, the vector further comprises a sequence encoding a fusion partner, linked to said polynucleotide to form a fusion protein upon  
20 expression. The fusion partner may be selected from the group consisting of human superoxide dismutase, ubiquitin, yeast  $\alpha$ -factor, IL-2S,  $\beta$ -galactosidase,  $\beta$ -lactamase, horseradish peroxidase, glucose oxidase and urease.

According to a sixth aspect of the invention, there is provided a method for assaying compounds for activity against hepatitis C virus, which  
25 method comprises:

(a) providing a protease derived from the NS3 region of hepatitis C virus;

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**2079105**

(b) contacting said protease with a compound capable of inhibiting serine protease activity; and

(c) measuring inhibition of the proteolytic activity of said protease.

**5    Brief Description of the Drawings**

Figure 1 shows the sequence of HCV protease.

Figure 2 shows the polynucleotide sequence and deduced amino acid sequence of the clone C20c.

Figure 3 shows the polynucleotide sequence and deduced amino acid sequence of the clone C26d.

Figure 4 shows the polynucleotide sequence and deduced amino acid sequence of the clone C8h.

Figure 5 shows the polynucleotide sequence and deduced amino acid sequence of the clone C7f.

Figure 6 shows the polynucleotide sequence and deduced amino acid sequence of the clone C31.

Figure 7 shows the polynucleotide sequence and deduced amino acid sequence of the clone C35.

Figure 8 shows the polynucleotide sequence and deduced amino acid sequence of the clone C33c.

Figure 9 schematically illustrates assembly of the vector C7fC20cC300C200.

Figure 10 shows the sequence of vector cf1SODp600.

Modes of Carrying Out The Invention

A. Definitions

5 The terms "Hepatitis C Virus" and "HCV" refer to the viral species that is the major etiological agent of BB-NANBH, the prototype isolate of which is identified in PCT WO89/046699; EPO publication 318,216.

10 "HCV" as used herein includes the pathogenic strains capable of causing hepatitis C, and attenuated strains or defective interfering particles derived therefrom. The HCV genome is comprised of RNA. It is known that RNA-containing viruses have relatively high rates of spontaneous mutation, reportedly on the order of  $10^{-3}$  to  $10^{-4}$  per incorporated nucleotide (Fields & Knipe, "Fundamental Virology" (1986, Raven Press, N.Y.)). As heterogeneity and fluidity of genotype are inherent characteristics of RNA viruses, there will be multiple strains/isolates, which may be virulent or avirulent, within the HCV species.

15 Information on several different strains/isolates of HCV is disclosed herein, particularly strain or isolate CDC/HCVI (also called HCV1). Information from one strain or isolate, such as a partial genomic sequence, is sufficient to allow those skilled in the art using standard techniques to isolate new strains/ isolates and to identify whether such new strains/isolates are HCV. For example, several different strains/isolates are described below. These strains, which were obtained from a number of human sera (and from different geographical areas), were isolated utilizing the information from the genomic sequence of HCV1.

25 The information provided herein suggests that HCV may be distantly related to the flaviviridae. The Flavivirus family contains a large number of viruses which are small, enveloped pathogens of man. The morphology and composition of Flavivirus particles are known, and are discussed in M.A. Brinton, in "The Viruses: The Togaviridae And Flaviviridae" (Series eds. Fraenkel-Conrat and

Wagner, vol. eds. Schlesinger and Schlesinger, Plenum Press, 1986), pp. 327-374. Generally, with respect to morphology, Flaviviruses contain a central nucleocapsid surrounded by a lipid bilayer. Virions are spherical and have a diameter of about 40-50 nm. Their cores are about 25-30 nm in diameter. Along the outer surface  
5 of the virion envelope are projections measuring about 5-10 nm in length with terminal knobs about 2 nm in diameter. Typical examples of the family include Yellow Fever virus, West Nile virus, and Dengue Fever virus. They possess positive-stranded RNA genomes (about 11,000 nucleotides) that are slightly larger than that of HCV and encode a polyprotein precursor of about 3500 amino acids.  
10 Individual viral proteins are cleaved from this precursor polypeptide.

The genome of HCV appears to be single-stranded RNA containing about 10,000 nucleotides. The genome is positive-stranded, and possesses a continuous translational open reading frame (ORF) that encodes a polyprotein of about 3,000 amino acids. In the ORF, the structural proteins appear to be  
15 encoded in approximately the first quarter of the N-terminal region, with the majority of the polyprotein attributed to non-structural proteins. When compared with all known viral sequences, small but significant co-linear homologies are observed with the non-structural proteins of the Flavivirus family, and with the pestiviruses (which are now also considered to be part of the Flavivirus family).  
20

The Yellow Fever Virus polyprotein contains, from the amino terminus to the carboxy terminus, the nucleocapsid protein (C), the matrix protein (M), the envelope protein (E), and the non-  
25 structural proteins 1, 2 (a+b), 3, 4 (a+b), and 5 (NS1, NS2, NS3, NS4, and NS5). Based upon the putative amino acids encoded in the nucleotide sequence of HCV1, a small domain at the extreme N-terminus of the HCV polyprotein

appears similar both in size and high content of basic residues to the nucleocapsid protein (C) found at the N-terminus of flaviviral polyproteins. The non-structural proteins 2,3,4, and 5 (NS2-5) of HCV and of yellow fever virus (YFV) appear to have counterparts of similar size and hydropathicity, although the amino acid sequences diverge. However, the region of HCV which would correspond to the regions of YFV polyprotein which contains the M, E, and NS1 protein not only differs in sequence, but also appears to be quite different in size and hydropathicity. Thus, while certain domains of the HCV genome may be referred to herein as, for example, NS1, or NS2, it should be understood that these designations are for convenience of reference only; there may be considerable differences between the HCV family and flaviviruses that have yet to be appreciated.

Due to the evolutionary relationship of the strains or isolates of HCV, putative HCV strains and isolates are identifiable by their homology at the polypeptide level. With respect to the isolates disclosed herein, new HCV strains or isolates are expected to be at least about 40% homologous, some more than about 70% homologous, and some even more than about 80% homologous: some may be more than about 90% homologous at the polypeptide level. The techniques for determining amino acid sequence homology are known in the art. For example, the amino acid sequence may be determined directly and compared to the sequences provided herein. Alternatively the nucleotide sequence of the genomic material of the putative HCV may be determined (usually via a cDNA intermediate), the amino acid sequence encoded therein can be determined, and the corresponding regions compared.

The term "HCV protease" refers to an enzyme derived from HCV which exhibits proteolytic activity, specifically the polypeptide encoded in the NS3 domain of the HCV genome. At least one strain of HCV contains a protease believed to be substantially encoded by or within the following sequence:

- 7 -

	Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro	10
	Ala Asp Gly Met Val Ser Lys Gly Trp Arg	20
	Leu Leu Ala Pro Ile Thr Ala Tyr Ala Gln	30
	Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile	40
5	Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln	50
	Val Glu Gly Glu Val Gln Ile Val Ser Thr	60
	Ala Ala Gln Thr Phe Leu Ala Thr Cys Ile	70
	Asn Gly Val Cys Trp Thr Val Tyr His Gly	80
	Ala Gly Thr Arg Thr Ile Ala Ser Pro Lys	90
10	Gly Pro Val Ile Gln Met Tyr Thr Asn Val	100
	Asp Gln Asp Leu Val Gly Trp Pro Ala Ser	110
	Gln Gly Thr Arg Ser Leu Thr Pro Cys Thr	120
	Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr	130
	Arg His Ala Asp Val Ile Pro Val Arg Arg	140
15	Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser	150
	Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser	160
	Ser Gly Gly Pro Leu Leu Cys Pro Ala Gly	170
	His Ala Val Gly Ile Phe Arg Ala Ala Val	180
	Cys Thr Arg Gly Val Ala Lys Ala Val Asp	190
20	Phe Ile Pro Val Glu Asn Leu Glu Thr Thr	200
	Met Arg ***	202

The above N and C termini are putative, the actual termini being defined by expression and processing in an appropriate host of a DNA construct encoding the entire NS3 domain. It is understood that this sequence may vary from strain to strain, as RNA viruses like HCV are known to exhibit a great deal of variation. Further, the actual N and C termini may vary, as the protease is cleaved from a precursor polyprotein: variations in the protease amino acid sequence can result in cleavage from the polyprotein at different points. Thus, the amino- and carboxy-termini may differ from strain to strain of HCV. The first amino acid shown above corresponds to residue 60 in Figure 1. However, the minimum sequence necessary for activity can be determined by routine methods. The sequence may be truncated at either end by treating an appropriate expression vector with an exonuclease (after cleavage at the 5' or 3' end of the coding sequence) to remove any desired number of base pairs. The resulting coding polynucleotide is then expressed and the sequence determined. In this manner

the activity of the resulting product may be correlated with the amino acid sequence: a limited series of such experiments (removing progressively greater numbers of base pairs) determines the minimum internal sequence necessary for protease activity. We have found that the sequence may be substantially truncated, particularly at the carboxy terminus, apparently with full retention of protease activity. It is presently believed that a portion of the protein at the carboxy terminus may exhibit helicase activity. However, helicase activity is not required of the HCV proteases of the invention. The amino terminus may also be truncated to a degree without loss of protease activity.

- 10 The amino acids underlined above are believed to be the residues necessary for catalytic activity, based on sequence homology to putative flavivirus serine proteases. Table 1 shows the alignment of the three serine protease catalytic residues for HCV protease and the protease obtained from Yellow Fever Virus, West Nile Fever virus, Murray Valley Fever virus, and Kunjin virus.
- 15 Although the other four flavivirus protease sequences exhibit higher homology with each other than with HCV, a degree of homology is still observed with HCV. This homology, however, was not sufficient for indication by currently available alignment software. The indicated amino acids are numbered His<sub>79</sub>, Asp<sub>103</sub>, and Ser<sub>161</sub> in the sequence listed above (His<sub>139</sub>, Asp<sub>163</sub>, and Ser<sub>221</sub> in Figure 1).

20

TABLE 1: Alignment of Active Residues by Sequence

Protease	His	Asp	Ser
25 HCV	CWTVY <u>H</u> GAG	DQDLGWPAP	LKGS <u>E</u> GGPL
Yellow Fever	FHTMWHVTR	KEDLVAYGG	PSGT <u>S</u> GSPI
West Nile Fever	FHTLW <u>H</u> TTK	KEDRLCYGG	PTGT <u>S</u> GSPI
Murray Valley	FHTLW <u>H</u> TTR	KEDRVTYGG	PIGT <u>S</u> GSPI
30 Kunjin Virus	FHTLW <u>H</u> TTK	KEDRLCYGG	PTGT <u>S</u> GSPI

Alternatively, one can make catalytic residue assignments based on structural homology. Table 2 shows alignment of HCV with against the catalytic sites of several well-characterized serine proteases based on structural considerations: protease A from *Streptomyces griseus*,  $\alpha$ -lytic protease, bovine trypsin, chymotrypsin, and elastase (M. James et al, Can J Biochem (1978) 56:396). Again, a degree of homology is observed. The HCV residues identified are numbered His<sub>78</sub>, Asp<sub>125</sub>, and Ser<sub>181</sub> in the sequence listed above.

TABLE 2: Alignment of Active Residues by Structure

Protease	His	Asp	Ser
<i>S. griseus</i> A	TAGHC	NNDYGII	GD\$GGSL
$\alpha$ -Lytic protease	TAGHC	GNDRAWV	GD\$GGSW
Bovine Trypsin	SAAHC	NNQIMLI	GD\$GGPV
Chymotrypsin	TAAHC	NNQITLL	GD\$GGPL
Elastase	TAAHC	GYDIALL	GD\$GGPL
HCV	TVYHG	SSDLYLV	G\$GGGPL

The most direct manner to verify the residues essential to the active site is to replace each residue individually with a residue of equivalent steric size. This is easily accomplished by site-specific mutagenesis and similar methods known in the art. If replacement of a particular residue with a residue of equivalent size results in loss of activity, the essential nature of the replaced residue is confirmed.

"HCV protease analogs" refer to polypeptides which vary from the full length protease sequence by deletion, alteration and/or addition to the amino acid sequence of the native protease. HCV protease analogs include the truncated proteases described above, as well as HCV protease muteins and fusion proteins comprising HCV protease, truncated protease, or protease muteins.



- 10 -

Alterations to form HCV protease muteins are preferably conservative amino acid substitutions, in which an amino acid is replaced with another naturally-occurring amino acid of similar character. For example, the following substitutions are considered "conservative":

5

Gly - Ala;

Val - Ile - Leu;

Asp - Glu;

Lys - Arg;

Asn - Gln; and

Phe - Trp - Tyr.

- 11 -

Nonconservative changes are generally substitutions of one of the above amino acids with an amino acid from a different group (e.g., substituting Asn for Glu), or substituting Cys, Met, His, or Pro for any of the above amino acids. Substitutions involving common amino acids are conveniently performed by site specific mutagenesis of an expression vector encoding the desired protein, and subsequent expression of the altered form. One may also alter amino acids by synthetic or semi-synthetic methods. For example, one may convert cysteine or serine residues to selenocysteine by appropriate chemical treatment of the isolated protein. Alternatively, one may incorporate uncommon amino acids in standard *in vitro* protein synthetic methods. Typically, the total number of residues changed, deleted or added to the native sequence in the muteins will be no more than about 20, preferably no more than about 10, and most preferably no more than about 5.

The term fusion protein generally refers to a polypeptide comprising an amino acid sequence drawn from two or more individual proteins. In the present invention, "fusion protein" is used to denote a polypeptide comprising the HCV protease, truncate, mutein or a functional portion thereof, fused to a non-HCV protein or polypeptide ("fusion partner"). Fusion proteins are most conveniently produced by expression of a fused gene, which encodes a portion of one polypeptide at the 5' end and a portion of a different polypeptide at the 3' end, where the different portions are joined in one reading frame which may be expressed in a suitable host. It is presently preferred (although not required) to position the HCV protease or analog at the carboxy terminus of the fusion protein, and to employ a functional enzyme fragment at the amino terminus. As the HCV protease is normally expressed within a large polyprotein, it is not expected to include cell transport signals (e.g., export or secretion signals). Suitable functional enzyme fragments are those polypeptides which exhibit a quantifiable activity when expressed fused to the HCV protease. Exemplary enzymes include, with-

- 12 -

out limitation,  $\beta$ -galactosidase ( $\beta$ -gal),  $\beta$ -lactamase, horseradish peroxidase (HRP), glucose oxidase (GO), human superoxide dismutase (hSOD), urease, and the like. These enzymes are convenient because the amount of fusion protein produced can be quantified by means of simple colorimetric assays. Alternatively, one may  
5 employ antigenic proteins or fragments, to permit simple detection and quantification of fusion proteins using antibodies specific for the fusion partner. The presently preferred fusion partner is hSOD.

#### B. General Method

10 The practice of the present invention generally employs conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See for example J. Sambrook et al, "Molecular Cloning; A Laboratory Manual (1989); "DNA Cloning", Vol. I and II (D.N Glover ed. 1985);  
15 "Oligonucleotide Synthesis" (M.J. Gait ed, 1984); "Nucleic Acid Hybridization" (B.D. Hames & S.J. Higgins eds. 1984); "Transcription And Translation" (B.D. Hames & S.J. Higgins eds. 1984); "Animal Cell Culture" (R.I. Freshney ed. 1986); "Immobilized Cells And Enzymes" (IRL Press, 1986); B. Perbal, "A Practical Guide To Molecular Cloning" (1984); the series, "Methods In Enzymology"  
20 (Academic Press, Inc.); "Gene Transfer Vectors For Mammalian Cells" (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Meth Enzymol (1987) 154 and 155 (Wu and Grossman, and Wu, eds., respectively); Mayer & Walker, eds. (1987), "Immunochemical Methods In Cell And Molecular Biology" (Academic Press, London); Scopes, "Protein Purification: Principles And  
25 Practice", 2nd Ed (Springer-Verlag, N.Y., 1987); and "Handbook Of Experimental Immunology", volumes I-IV (Weir and Blackwell, eds, 1986).

Both prokaryotic and eukaryotic host cells are useful for expressing desired coding sequences when appropriate control sequences compatible with the

designated host are used. Among prokaryotic hosts, *E. coli* is most frequently used. Expression control sequences for prokaryotes include promoters, optionally containing operator portions, and ribosome binding sites. Transfer vectors compatible with prokaryotic hosts are commonly derived from, for example, pBR322, 5 a plasmid containing operons conferring ampicillin and tetracycline resistance, and the various pUC vectors, which also contain sequences conferring antibiotic resistance markers. These plasmids are commercially available. The markers may be used to obtain successful transformants by selection. Commonly used prokaryotic control sequences include the  $\beta$ -lactamase (penicillinase) and lactose promoter 10 systems (Chang et al, Nature (1977) 198:1056), the tryptophan (*trp*) promoter system (Goeddel et al, Nuc Acids Res (1980) 8:4057) and the lambda-derived  $P_L$  promoter and N gene ribosome binding site (Shimatake et al, Nature (1981) 292:128) and the hybrid *lac* promoter (De Boer et al, Proc Nat Acad Sci USA (1983) 292:128) derived from sequences of the *trp* and *lac* UV5 promoters. The 15 foregoing systems are particularly compatible with *E. coli*; if desired, other prokaryotic hosts such as strains of *Bacillus* or *Pseudomonas* may be used, with corresponding control sequences.

Eukaryotic hosts include without limitation yeast and mammalian cells in culture systems. Yeast expression hosts include *Saccharomyces*, *Klebsiella*, 20 *Picia*, and the like. *Saccharomyces cerevisiae* and *Saccharomyces carlsbergensis* and *K. lactis* are the most commonly used yeast hosts, and are convenient fungal hosts. Yeast-compatible vectors carry markers which permit selection of successful transformants by conferring prototrophy to auxotrophic mutants or resistance to heavy metals on wild-type strains. Yeast compatible vectors may employ the  $2\mu$  origin 25 of replication (Broach et al, Meth Enzymol (1983) 101:307), the combination of CEN3 and ARS1 or other means for assuring replication, such as sequences which will result in incorporation of an appropriate fragment into the host cell genome. Control sequences for yeast vectors are known in the art and include promoters

for the synthesis of glycolytic enzymes (Hess et al, J Adv Enzyme Reg (1968) 7: 149; Holland et al, Biochem (1978), 17:4900), including the promoter for 3-phosphoglycerate kinase (R. Hitzeman et al, J Biol Chem (1980) 255:2073). Terminators may also be included, such as those derived from the enolase gene (Holland, 5 J Biol Chem (1981) 256:1385). Particularly useful control systems are those which comprise the glyceraldehyde-3 phosphate dehydrogenase (GAPDH) promoter or alcohol dehydrogenase (ADH) regulatable promoter, terminators also derived from GAPDH, and if secretion is desired, a leader sequence derived from yeast  $\alpha$ -factor (see U.S. Pat. No. 4,870,008, incorporated herein by reference).

10 A presently preferred expression system employs the ubiquitin leader as the fusion partner.

Yeast ubiquitin provides a 76 amino acid polypeptide which is automatically cleaved from the fused protein upon expression. The ubiquitin amino acid 15 sequence is as follows:

20 Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr  
Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val  
Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp  
Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu  
Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys  
Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly  
Gly

See also Ozkaynak et al, Nature (1984) 312:663-66. Polynucleotides 25 encoding the ubiquitin polypeptide may be synthesized by standard methods, for example following the technique of Barr et al, J Biol Chem (1988) 268:1671-78 using an Applied Biosystem 380A DNA synthesizer. Using appropriate linkers, the ubiquitin gene may be inserted into a suitable vector and ligated to a sequence encoding the HCV protease or a fragment thereof.

In addition, the transcriptional regulatory region and the transcriptional initiation region which are operably linked may be such that they are not naturally associated in the wild-type organism. These systems are described in detail in EPO 120,551, published October 3, 1984; EPO 116,201, published August 22, 1984; and EPO 164,556, published December 18, 1985, all of which are commonly owned with the present invention.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including HeLa cells, Chinese hamster ovary (CHO) cells, baby hamster kidney (BHK) cells, and a number of other cell lines. Suitable promoters for mammalian cells are also known in the art and include viral promoters such as that from Simian Virus 40 (SV40) (Fiers et al, Nature (1978) 273:113), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences and poly-A addition sequences. Enhancer sequences which increase expression may also be included, and sequences which promote amplification of the gene may also be desirable (for example methotrexate resistance genes). These sequences are known in the art.

Vectors suitable for replication in mammalian cells are known in the art, and may include viral replicons, or sequences which insure integration of the appropriate sequences encoding HCV epitopes into the host genome. For example, another vector used to express foreign DNA is Vaccinia virus. In this case the heterologous DNA is inserted into the Vaccinia genome. Techniques for the insertion of foreign DNA into the vaccinia virus genome are known in the art, and may utilize, for example, homologous recombination. The heterologous DNA is generally inserted into a gene which is non-essential to the virus, for example, the thymidine kinase gene (tk), which also provides a selectable marker. Plasmid

vectors that greatly facilitate the construction of recombinant viruses have been described (see, for example, Mackett et al, J Virol (1984) 49:857; Chakrabarti et al, Mol Cell Biol (1985) 5:3403; Moss, in GENE TRANSFER VECTORS FOR MAMMALIAN CELLS (Miller and Calos, eds., Cold Spring Harbor Laboratory, NY, 1987), p. 10). Expression of the HCV polypeptide then occurs in cells or animals which are infected with the live recombinant vaccinia virus.

In order to detect whether or not the HCV polypeptide is expressed from the vaccinia vector, BSC 1 cells may be infected with the recombinant vector and grown on microscope slides under conditions which allow expression. The cells may then be acetone-fixed, and immunofluorescence assays performed using serum which is known to contain anti-HCV antibodies to a polypeptide(s) encoded in the region of the HCV genome from which the HCV segment in the recombinant expression vector was derived.

Other systems for expression of eukaryotic or viral genomes include insect cells and vectors suitable for use in these cells. These systems are known in the art, and include, for example, insect expression transfer vectors derived from the baculovirus *Autographa californica* nuclear polyhedrosis virus (AcNPV), which is a helper-independent, viral expression vector. Expression vectors derived from this system usually use the strong viral polyhedrin gene promoter to drive expression of heterologous genes. Currently the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373 (see PCT WO89/046699). Many other vectors known to those of skill in the art have also been designed for improved expression. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and introduces a BamHI cloning site 32 bp downstream from the ATT; See Luckow and Summers, Virology (1989) 17:31). AcNPV transfer vectors for high level expression of nonfused foreign proteins are described in copending applications PCT WO89/046699 and USSN 7/456,637. A unique BamHI site is located following

position -8 with respect to the translation initiation codon ATG of the polyhedrin gene. There are no cleavage sites for SmaI, PstI, BglII, XbaI or SstI. Good expression of nonfused foreign proteins usually requires foreign genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. The plasmid also contains the polyhedrin polyadenylation signal and the ampicillin-resistance (amp) gene and origin of replication for selection and propagation in *E. coli*.

Methods for the introduction of heterologous DNA into the desired site in the baculovirus virus are known in the art. (See Summer and Smith, Texas Agricultural Experiment Station Bulletin No. 1555; Smith et al, Mol Cell Biol (1983) 3:2156-2165; and Luckow and Summers, Virology (1989) 17:31). For example, the heterologous DNA can be inserted into a gene such as the polyhedrin gene by homologous recombination, or into a restriction enzyme site engineered into the desired baculovirus gene. The inserted sequences may be those which encode all or varying segments of the polyprotein, or other orfs which encode viral polypeptides. For example, the insert could encode the following numbers of amino acid segments from the polyprotein: amino acids 1-1078; amino acids 332-662; amino acids 406-662; amino acids 156-328, and amino acids 199-328.

The signals for post-translational modifications, such as signal peptide cleavage, proteolytic cleavage, and phosphorylation, appear to be recognized by insect cells. The signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells. Examples of the signal sequences from vertebrate cells which are effective in invertebrate cells are known in the art, for example, the human interleukin-2 signal (IL2<sub>s</sub>) which signals for secretion from the cell, is recognized and properly removed in insect cells.

Transformation may be by any known method for introducing polynucleotides into a host cell, including, for example packaging the polynucleotide in



a virus and transducing a host cell with the virus, and by direct uptake of the polynucleotide. The transformation procedure used depends upon the host to be transformed. Bacterial transformation by direct uptake generally employs treatment with calcium or rubidium chloride (Cohen, Proc Nat Acad Sci USA (1972) 69:2110; T. Maniatis et al, "Molecular Cloning; A Laboratory Manual" (Cold Spring Harbor Press, Cold Spring Harbor, NY, 1982). Yeast transformation by direct uptake may be carried out using the method of Hinnen et al, Proc Nat Acad Sci USA (1978) 75:1929. Mammalian transformations by direct uptake may be conducted using the calcium phosphate precipitation method of Graham and Van der Eb, Virology (1978) 52:546, or the various known modifications thereof. Other methods for introducing recombinant polynucleotides into cells, particularly into mammalian cells, include dextran-mediated transfection, calcium phosphate mediated transfection, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the polynucleotides into nuclei.

Vector construction employs techniques which are known in the art. Site-specific DNA cleavage is performed by treating with suitable restriction enzymes under conditions which generally are specified by the manufacturer of these commercially available enzymes. In general, about 1  $\mu$ g of plasmid or DNA sequence is cleaved by 1 unit of enzyme in about 20  $\mu$ L buffer solution by incubation for 1-2 hr at 37°C. After incubation with the restriction enzyme, protein is removed by phenol/chloroform extraction and the DNA recovered by precipitation with ethanol. The cleaved fragments may be separated using polyacrylamide or agarose gel electrophoresis techniques, according to the general procedures described in Meth Enzymol (1980) 65:499-560.

Sticky-ended cleavage fragments may be blunt ended using *E. coli* DNA polymerase I (Klenow fragment) with the appropriate deoxynucleotide tri-

phosphates (dNTPs) present in the mixture. Treatment with S1 nuclease may also be used, resulting in the hydrolysis of any single stranded DNA portions.

5 Ligations are carried out under standard buffer and temperature conditions using T4 DNA ligase and ATP; sticky end ligations require less ATP and less ligase than blunt end ligations. When vector fragments are used as part of a ligation mixture, the vector fragment is often treated with bacterial alkaline phosphatase (BAP) or calf intestinal alkaline phosphatase to remove the 5'-phosphate, thus preventing religation of the vector. Alternatively, restriction enzyme digestion of unwanted fragments can be used to prevent ligation.

10 Ligation mixtures are transformed into suitable cloning hosts, such as *E. coli*, and successful transformants selected using the markers incorporated (e.g., antibiotic resistance), and screened for the correct construction.

Synthetic oligonucleotides may be prepared using an automated oligonucleotide synthesizer as described by Warner, DNA (1984) 3:401. If  
15 desired, the synthetic strands may be labeled with  $^{32}\text{P}$  by treatment with polynucleotide kinase in the presence of  $^{32}\text{P}$ -ATP under standard reaction conditions.

DNA sequences, including those isolated from cDNA libraries, may be modified by known techniques, for example by site directed mutagenesis (see e.g., Zoller, Nuc Acids Res (1982) 10:6487). Briefly, the DNA to be modified is  
20 packaged into phage as a single stranded sequence, and converted to a double stranded DNA with DNA polymerase, using as a primer a synthetic oligonucleotide complementary to the portion of the DNA to be modified, where the desired modification is included in the primer sequence. The resulting double stranded DNA is transformed into a phage-supporting host bacterium. Cultures of the  
25 transformed bacteria which contain copies of each strand of the phage are plated in agar to obtain plaques. Theoretically, 50% of the new plaques contain phage having the mutated sequence, and the remaining 50% have the original sequence. Replicates of the plaques are hybridized to labeled synthetic probe at temper-

- 20 -

atures and conditions which permit hybridization with the correct strand, but not with the unmodified sequence. The sequences which have been identified by hybridization are recovered and cloned.

DNA libraries may be probed using the procedure of Grunstein and  
5 Hogness Proc Nat Acad Sci USA (1975) 73:3961. Briefly, in this procedure the DNA to be probed is immobilized on nitrocellulose filters, denatured, and prehybridized with a buffer containing 0-50% formamide, 0.75 M NaCl, 75 mM Na citrate, 0.02% (wt/v) each of bovine serum albumin, polyvinylpyrrolidone, and Ficoll®, 50 mM NaH<sub>2</sub>PO<sub>4</sub> (pH 6.5), 0.1% SDS, and 100 µg/mL carrier denatured  
10 DNA. The percentage of formamide in the buffer, as well as the time and temperature conditions of the prehybridization and subsequent hybridization steps depend on the stringency required. Oligomeric probes which require lower stringency conditions are generally used with low percentages of formamide, lower temperatures, and longer hybridization times. Probes containing more than 30 or  
15 40 nucleotides, such as those derived from cDNA or genomic sequences generally employ higher temperatures, e.g., about 40-42°C, and a high percentage formamide, e.g., 50%. Following prehybridization, 5'-<sup>32</sup>P-labeled oligonucleotide probe is added to the buffer, and the filters are incubated in this mixture under hybridization conditions. After washing, the treated filters are subjected to  
20 autoradiography to show the location of the hybridized probe; DNA in corresponding locations on the original agar plates is used as the source of the desired DNA.

For routine vector constructions, ligation mixtures are transformed  
into *E. coli* strain HB101 or other suitable hosts, and successful transformants selected by antibiotic resistance or other markers. Plasmids from the transformants  
25 are then prepared according to the method of Clewell et al, Proc Nat Acad Sci USA (1969) 62:1159, usually following chloramphenicol amplification (Clewell, J Bacteriol (1972) 110:667). The DNA is isolated and analyzed, usually by restric-

- 21 -

tion enzyme analysis and/or sequencing. Sequencing may be performed by the dideoxy method of Sanger et al, Proc Nat Acad Sci USA (1977) 74:5463, as further described by Messing et al, Nuc Acids Res (1981) 9:309, or by the method of Maxam et al, Meth Enzymol (1980) 65:499. Problems with band compression, which are sometimes observed in GC-rich regions, were overcome by use of T-deazoguanosine according to Barr et al, Biotechniques (1986) 4:428.

The enzyme-linked immunosorbent assay (ELISA) can be used to measure either antigen or antibody concentrations. This method depends upon conjugation of an enzyme to either an antigen or an antibody, and uses the bound enzyme activity as a quantitative label. To measure antibody, the known antigen is fixed to a solid phase (e.g., a microtiter dish, plastic cup, dipstick, plastic bead, or the like), incubated with test serum dilutions, washed, incubated with anti-immunoglobulin labeled with an enzyme, and washed again. Enzymes suitable for labeling are known in the art, and include, for example, horseradish peroxidase (HRP). Enzyme activity bound to the solid phase is usually measured by adding a specific substrate, and determining product formation or substrate utilization colorimetrically. The enzyme activity bound is a direct function of the amount of antibody bound.

To measure antigen, a known specific antibody is fixed to the solid phase, the test material containing antigen is added, after an incubation the solid phase is washed, and a second enzyme-labeled antibody is added. After washing, substrate is added, and enzyme activity is measured colorimetrically, and related to antigen concentration.

Proteases of the invention may be assayed for activity by cleaving a substrate which provides detectable cleavage products. As the HCV protease is believed to cleave itself from the genomic polyprotein, one can employ this autocatalytic activity both to assay expression of the protein and determine activity. For example, if the protease is joined to its fusion partner so that the HCV pro-

- 22 -

tease N-terminal cleavage signal (Arg-Arg) is included, the expression product will cleave itself into fusion partner and active HCV protease. One may then assay the products, for example by western blot, to verify that the proteins produced correspond in size to the separate fusion partner and protease proteins. It is presently preferred to employ small peptide p-nitrophenyl esters or methylcoumarins, as cleavage may then be followed by spectrophotometric or fluorescent assays. Following the method described by E.D. Matayoshi et al, Science (1990) 247:231-35, one may attach a fluorescent label to one end of the substrate and a quenching molecule to the other end: cleavage is then determined by measuring the resulting increase in fluorescence. If a suitable enzyme or antigen has been employed as the fusion partner, the quantity of protein produced may easily be determined. Alternatively, one may exclude the HCV protease N-terminal cleavage signal (preventing self-cleavage) and add a separate cleavage substrate, such as a fragment of the HCV NS3 domain including the native processing signal or a synthetic analog.

In the absence of this protease activity, the HCV polyprotein should remain in its unprocessed form, and thus render the virus noninfectious. Thus, the protease is useful for assaying pharmaceutical agents for control of HCV, as compounds which inhibit the protease activity sufficiently will also inhibit viral infectivity. Such inhibitors may take the form of organic compounds, particularly compounds which mimic the cleavage site of HCV recognized by the protease. Three of the putative cleavage sites of the HCV polyprotein have the following amino acid sequences:

Val-Ser-Ala-Arg-Arg // Gly-Arg-Glu-Ile-Leu-Leu-Gly  
Ala-Ile-Leu-Arg-Arg // His-Val-Gly-Pro-  
Val-Ser-Cys-Gln-Arg // Gly-Tyr-

These sites are characterized by the presence of two basic amino acids immediately before the cleavage site, and are similar to the cleavage sites recognized by other flavivirus proteases. Thus, suitable protease inhibitors may be prepared which mimic the basic/basic/small neutral motif of the HCV cleavage sites, but substituting a nonlabile linkage for the peptide bond cleaved in the natural substrate. Suitable inhibitors include peptide trifluoromethyl ketones, peptide boronic acids, peptide  $\alpha$ -ketoesters, peptide difluoroketo compounds, peptide aldehydes, peptide diketones, and the like. For example, the peptide aldehyde N-acetyl-phenylalanyl-glycinaldehyde is a potent inhibitor of the protease papain. One may conveniently prepare and assay large mixtures of peptides using the methods disclosed in

PCT WO89/10931. This application teaches methods for generating mixtures of peptides up to hexapeptides having all possible amino acid sequences, and further teaches assay methods for identifying those peptides capable of binding to proteases.

Other protease inhibitors may be proteins, particularly antibodies and antibody derivatives. Recombinant expression systems may be used to generate quantities of protease sufficient for production of monoclonal antibodies (MAbs) specific for the protease. Suitable antibodies for protease inhibition will bind to the protease in a manner reducing or eliminating the enzymatic activity, typically by obscuring the active site. Suitable MAbs may be used to generate derivatives, such as Fab fragments, chimeric antibodies, altered antibodies, univalent antibodies, and single domain antibodies, using methods known in the art.

Protease inhibitors are screened using methods of the invention. In general, a substrate is employed which mimics the enzyme's natural substrate, but which provides a quantifiable signal when cleaved. The signal is preferably detectable by colorimetric or fluorometric means: however, other methods such as HPLC or silica gel chromatography, GC-MS, nuclear magnetic resonance, and

the like may also be useful. After optimum substrate and enzyme concentrations are determined, a candidate protease inhibitor is added to the reaction mixture at a range of concentrations. The assay conditions ideally should resemble the conditions under which the protease is to be inhibited *in vivo*, i.e., under physiologic  
5 pH, temperature, ionic strength, etc. Suitable inhibitors will exhibit strong protease inhibition at concentrations which do not raise toxic side effects in the subject. Inhibitors which compete for binding to the protease active site may require concentrations equal to or greater than the substrate concentration, while inhibitors capable of binding irreversibly to the protease active site may be added in  
10 concentrations on the order of the enzyme concentration.

In a presently preferred embodiment, an inactive protease mutein is employed rather than an active enzyme. It has been found that replacing a critical residue within the active site of a protease (e.g., replacing the active site Ser of a serine protease) does not significantly alter the structure of the enzyme,  
15 and thus preserves the binding specificity. The altered enzyme still recognizes and binds to its proper substrate, but fails to effect cleavage. Thus, in one method of the invention an inactivated HCV protease is immobilized, and a mixture of candidate inhibitors added. Inhibitors that closely mimic the enzyme's preferred recognition sequence will compete more successfully for binding than other candidate  
20 inhibitors. The poorly-binding candidates may then be separated, and the identity of the strongly-binding inhibitors determined. For example, HCV protease may be prepared substituting Ala for Ser<sub>221</sub> (Fig. 1), providing an enzyme capable of binding the HCV protease substrate, but incapable of cleaving it. The resulting protease mutein is then bound to a solid support, for example Sephadex®  
25 beads, and packed into a column. A mixture of candidate protease inhibitors in solution is then passed through the column and fractions collected. The last fractions to elute will contain the strongest-binding compounds, and provide the preferred protease inhibitor candidates.

Protease inhibitors may be administered by a variety of methods, such as intravenously, orally, intramuscularly, intraperitoneally, bronchially, intranasally, and so forth. The preferred route of administration will depend upon the nature of the inhibitor. Inhibitors prepared as organic compounds may often be administered orally (which is generally preferred) if well absorbed. Protein-based inhibitors (such as most antibody derivatives) must generally be administered by parenteral routes.

C. Examples

The examples presented below are provided as a further guide to the practitioner of ordinary skill in the art, and are not to be construed as limiting the invention in any way.

Example 1

(Preparation of HCV cDNA)

A genomic library of HCV cDNA was prepared as described in PCT WO89/046699. This library, ATCC accession no. 40394, has been deposited as set forth below.

Example 2

(Expression of the Polypeptide Encoded in Clone 5-1-1.)

(A) The HCV polypeptide encoded within clone 5-1-1 (see Example 1) was expressed as a fusion polypeptide with human superoxide dismutase (SOD). This was accomplished by subcloning the clone 5-1-1 cDNA insert into the expression vector pSODCF1 (K.S. Steimer et al, J Virol (1986) 58:9; EPO 138,111) as follows. The SOD/5-1-1 expression vector was transformed into *E. coli* D1210 cells. These cells, named Cf1/5-1-1 in *E. coli*, were deposited as set forth below and have an ATCC accession no. of 67967.



- 26 -

First, DNA isolated from pSODCF1 was treated with BamHI and EcoRI, and the following linker was ligated into the linear DNA created by the restriction enzymes:

GAT CCT GGA ATT CTG ATA AGA CCT TAA GAC TAT TTT AA

5

After cloning, the plasmid containing the insert was isolated.

Plasmid containing the insert was restricted with EcoRI. The HCV cDNA insert in clone 5-1-1 was excised with EcoRI, and ligated into this EcoRI linearized plasmid DNA. The DNA mixture was used to transform *E. coli* strain D1210 (Sadler et al, Gene (1980) 8:279). Recombinants with the 5-1-1 cDNA in the correct orientation for expressing the ORF shown in Figure 1 were identified by restriction mapping and nucleotide sequencing.

5

Recombinant bacteria from one clone were induced to express the SOD-HCV<sub>5-1-1</sub> polypeptide by growing the bacteria in the presence of IPTG.

10

Three separate expression vectors, pcf1AB, pcf1CD, and pcf1EF were created by ligating three new linkers, AB, CD, and EF to a BamHI-EcoRI fragment derived by digesting to completion the vector pSODCF1 with EcoRI and BamHI, followed by treatment with alkaline phosphatase. The linkers were created from six oligomers, A, B, C, D, E, and F. Each oligomer was phosphorylated by treatment with kinase in the presence of ATP prior to annealing to its complementary oligomer. The sequences of the synthetic linkers were the following:

15

- 27 -

	Name	DNA Sequence (5' to 3')
5	A	GATC CTG AAT TCC TGA TAA
	B	GAC TTA AGG ACT ATT TTA A
	C	GATC CGA ATT CTG TGA TAA
	D	GCT TAA GAC ACT ATT TTA A
10	E	GATC CTG GAA TTC TGA TAA
	F	GAC CTT AAG ACT ATT TTA A

Each of the three linkers destroys the original EcoRI site, and creates a new EcoRI site within the linker, but within a different reading frame. Thus, the HCV cDNA EcoRI fragments isolated from the clones, when inserted into the expression vector, were in three different reading frames.

The HCV cDNA fragments in the designated gt11 clones were excised by digestion with EcoRI; each fragment was inserted into pcf1AB, pcf1CD, and pcf1EF. These expression constructs were then transformed into D1210 *E. coli* cells, the transformants cloned, and polypeptides expressed as described in part B below.

(B) Expression products of the indicated HCV cDNAs were tested for antigenicity by direct immunological screening of the colonies, using a modification of the method described in Helfman et al, Proc Nat Acad Sci USA (1983), 80:31. Briefly, the bacteria were plated onto nitrocellulose filters overlaid on ampicillin plates to give approximately 40 colonies per filter. Colonies were replica plated onto nitrocellulose filters, and the replicas were regrown overnight in the presence of 2 mM IPTG and ampicillin. The bacterial colonies were lysed by suspending the nitrocellulose filters for about 15 to 20 min in an atmosphere saturated with  $\text{CHCl}_3$  vapor. Each filter then was placed in an individual 100 mm Petri dish containing 10 mL of 50 mM Tris HCl, pH 7.5, 150 mM NaCl, 5 mM  $\text{MgCl}_2$ , 3% (w/v) BSA, 40  $\mu\text{g/mL}$  lysozyme, and 0.1  $\mu\text{g/mL}$  DNase. The plates

- 28 -

were agitated gently for at least 8 hours at room temperature. The filters were rinsed in TBST (50 mM Tris HCl, pH 8.0, 150 mM NaCl, 0.005% Tween® 20). After incubation, the cell residues were rinsed and incubated for one hour in TBS (TBST without Tween®) containing 10% sheep serum. The filters were then

5 incubated with pretreated sera in TBS from individuals with NANBH, which included 3 chimpanzees; 8 patients with chronic NANBH whose sera were positive with respect to antibodies to HCV C100-3 polypeptide (also called C100); 8 patients with chronic NANBH whose sera were negative for anti-C100 antibodies; a convalescent patient whose serum was negative for anti-C100 antibodies; and 6

10 patients with community-acquired NANBH, including one whose sera was strongly positive with respect to anti-C100 antibodies, and one whose sera was marginally positive with respect to anti-C100 antibodies. The sera, diluted in TBS, was pre-treated by preabsorption with hSOD for at least 30 minutes at 37°C. After incubation, the filters were washed twice for 30 min with TBST. The expressed pro-

15 teins which bound antibodies in the sera were labeled by incubation for 2 hours with <sup>125</sup>I-labeled sheep anti-human antibody. After washing, the filters were washed twice for 30 min with TBST, dried, and autoradiographed.

### Example 3

20 (Cloning of Full-Length SOD-Protease Fusion Proteins)

(A) pBR322-C200:

The nucleotide sequences of the HCV cDNAs used below were determined essentially as described above, except that the cDNA excised from these phages were substituted for the cDNA isolated from clone 5-1-1.

25 Clone C33c was isolated using a hybridization probe having the following sequence:

5' ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT 3'

- 29 -

The sequence of the HCV cDNA in clone C33c is shown in Figure 8, which also shows the amino acids encoded therein.

Clone 35 was isolated by screening with a synthetic polynucleotide having the sequence:

5        5' AAG CCA CCG TGT GCG CTA GGG CTC AAG CCC 3'

Approximately 1 in 50,000 clones hybridized with the probe. The polynucleotide and deduced amino acid sequences for C35 are shown in Figure 7.

Clone C31 is shown in Figure 6, which also shows the amino acids encoded therein. A C200 cassette was constructed by ligating together a 718 bp fragment obtained by digestion of clone C33c DNA with EcoRI and HinfI, a 179 bp fragment obtained by digestion of clone C31 DNA with HinfI and BglI, and a 377 bp fragment obtained by digesting clone C35 DNA with BglI and EcoRI. The construct of ligated fragments were inserted into the EcoRI site of pBR322, yielding the plasmid pBR322-C200.

15            (B)        C7f+C20c:

Clone 7f was isolated using a probe having the sequence:

5'-AGC AGA CAA GGG GCC TCC TAG GGT GCA TAA T-3'

The sequence of HCV cDNA in clone 7f and the amino acids encoded therein are shown in Figure 5.

20            Clone C20c is isolated using a probe having the following sequence:

5'-TGC ATC AAT GGG GTG TGC TGG-3'

The sequence of HCV cDNA in clone C20c, and the amino acids encoded therein are shown in Figure 2.

25            Clones 7f and C20c were digested with EcoRI and SfaNI to form 400 bp and 260 bp fragments, respectively. The fragments were then cloned into the EcoRI site of pBR322 to form the vector C7f+C20c, and transformed into HB101 cells.

- 30 -

(C) C300:

Clone 8h was isolated using a probe based on the sequence of nucleotides in clone 33c. The nucleotide sequence of the probe was

5'-AGA GAC AAC CAT GAG GTC CCC GGT GTT C-3'.

- 5 The sequence of the HCV cDNA in clone 8h, and the amino acids encoded therein, are shown in Figure 4.

Clone C26d is isolated using a probe having the following sequence:

5'-CTG TTG TGC CCC GCG GCA GCC-3'

- 10 The sequence and amino acid translation of clone C26d is shown in Figure 3.

- Clones C26d and C33c (see part A above) were transformed into the methylation minus *E. coli* strain GM48. Clone C26d was digested with EcoRII and DdeI to provide a 100 bp fragment. Clone C33c was digested with EcoRII and EcoRI to provide a 700 bp fragment. Clone C8h was digested with  
15 EcoRI and DdeI to provide a 208 bp fragment. These three fragments were then ligated into the EcoRI site of pBR322, and transformed into *E. coli* HB101, to provide the vector C300.

(D) Preparation of Full Length Clones:

- 20 A 600 bp fragment was obtained from C7f+C20c by digestion with EcoRI and NaeI, and ligated to a 945 bp NaeI/EcoRI fragment from C300, and the construct inserted into the EcoRI site of pGEM4Z (commercially available from Promega) to form the vector C7fC20cC300.

- 25 C7fC20cC300 was digested with NdeI and EcoRI to provide a 892 bp fragment, which was ligated with a 1160 bp fragment obtained by digesting C200 with NdeI and EcoRI. The resulting construct was inserted into the EcoRI site of pBR322 to provide the vector C7fC20cC300C200. Construction of this vector is illustrated schematically in Figure 9.

Example 4(Preparation of *E. coli* Expression Vectors)(A) cf1SODp600:

This vector contains a full-length HCV protease coding sequence  
5 fused to a functional hSOD leader. The vector C7fC20cC300C200 was cleaved  
with EcoRI to provide a 2000 bp fragment, which was then ligated into the EcoRI  
site of plasmid cf1CD (Example 2A). The resulting vector encodes amino acids 1-  
151 of hSOD, and amino acids 946-1630 of HCV (numbered from the beginning  
of the polyprotein, corresponding to amino acids 1-686 in Figure 1). The vector  
10 was labeled cf1SODp600 (sometimes referred to as P600), and was transformed  
into *E. coli* D1210 cells. These cells, ATCC accession no. 68275, were deposited  
as set forth below.

(B) P190:

A truncated SOD-protease fusion polynucleotide was prepared by  
15 excising a 600 bp EcoRI/NaeI fragment from C7f+C20c, blunting the fragment  
with Klenow fragment, ligating the blunted fragment into the Klenow-blunted  
EcoRI site of cf1EF (Example 2A). This polynucleotide encodes a fusion protein  
having amino acids 1-151 of hSOD, and amino acids 1-199 of HCV protease.

(C) P300:

20 A longer truncated SOD-protease fusion polynucleotide was pre-  
pared by excising an 892 bp EcoRI/NdeI fragment from C7fC20cC300, blunting  
the fragment with Klenow fragment, ligating the blunted fragment into the  
Klenow-blunted EcoRI site of cf1EF. This polynucleotide encodes a fusion pro-  
tein having amino acids 1-151 of hSOD, and amino acids 1-299 of HCV protease.

25 (D) P500:

A longer truncated SOD-protease fusion polynucleotide was pre-  
pared by excising a 1550 bp EcoRI/EcoRI fragment from C7fC20cC300, and ligat-  
ing the fragment into the EcoRI site of cf1CD to form P500. This polynucleotide

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- 32 -

encodes a fusion protein having amino acids 1-151 of hSOD, and amino acids 946-1457 of HCV protease (amino acids 1-513 in Figure 1).

(E) FLAG/Protease Fusion

This vector contains a full-length HCV protease coding sequence fused to the FLAG sequence, Hopp et al. (1988) Biotechnology 6: 1204-1210. PCR was used to produce a HCV protease gene with special restriction ends for cloning ease. Plasmid p500 was digested with EcoRI and NdeI to yield a 900 bp fragment. This fragment and two primers were used in a polymerase chain reaction to introduce a unique BglII site at amino acid 1009 and a stop codon with a SalI site at amino acid 1262 of the HCV-1, as shown in Figure 17 of WO 90/11089, published 4 October 1990. The sequence of the primers is as follows:

5' CCC GAG CAA GAT CTC CCG GCC C 3'

and

5' CCC GGC TGC ATA AGC AGT CGA CTT GGA 3'

After 30 cycles of PCR, the reaction was digested with BglII and SalI, and the 710 bp fragment was isolated. This fragment was annealed and ligated to the following duplex:

MetAspTyrLysAspAspAspLysGlyArgGlu  
CATGGACTACAAAGACGATGACGATAAAGGCCGGGA  
CTGATGTTTCTGCTACTGCTATTTCCGGCCCTCTAG

The duplex encodes the FLAG sequence, and initiator methionine, and a 5' NcoI restriction site. The resulting NcoI/SalI fragment was ligated into a derivative of pCF1.

This construct is then transformed into *E. coli* D1210 cells and expression of the protease is induced by the addition of IPTG.

The FLAG sequence was fused to the HCV protease to facilitate purification. A calcium dependent monoclonal antibody, which binds to the

- 33 -

FLAG encoded peptide, is used to purify the fusion protein without harsh eluting conditions.

#### Example 5

##### 5 (E. coli Expression of SOD-Protease Fusion Proteins)

(A) *E. coli* D1210 cells were transformed with cf1SODp600 and grown in Luria broth containing 100 µg/mL ampicillin to an OD of 0.3-0.5. IPTG was then added to a concentration of 2 mM, and the cells cultured to a final OD of 0.9 to 1.3. The cells were then lysed, and the lysate analyzed by Western blot using anti-  
10 HCV sera, as described in USSN 7/456,637.

The results indicated the occurrence of cleavage, as no full length product (theoretical Mr 93 kDa) was evident on the gel. Bands corresponding to the hSOD fusion partner and the separate HCV protease appeared at relative molecular weights of about 34, 53, and 66 kDa. The 34 kDa band corresponds to the  
15 hSOD partner (about 20 kDa) with a portion of the NS3 domain, while the 53 and 66 kDa bands correspond to HCV protease with varying degrees of (possibly bacterial) processing.

(B) *E. coli* D1210 cells were transformed with P500 and grown in Luria broth containing 100 µg/mL ampicillin to an OD of 0.3-0.5. IPTG was then  
20 added to a concentration of 2 mM, and the cells cultured to a final OD of 0.8 to 1.0. The cells were then lysed, and the lysate analyzed as described above.

The results again indicated the occurrence of cleavage, as no full length product (theoretical Mr 73 kDa) was evident on the gel. Bands corresponding to the hSOD fusion partner and the truncated HCV protease appeared at molecular  
25 weights of about 34 and 45 kDa, respectively.

(C) *E. coli* D1210 cells were transformed with vectors P300 and P190 and grown as described above.



- 34 -

The results from P300 expression indicated the occurrence of cleavage, as no full length product (theoretical Mr 51 kDa) was evident on the gel. A band corresponding to the hSOD fusion partner appeared at a relative molecular weight of about 34. The corresponding HCV protease band was not visible, as this region of the NS3 domain is not recognized by the sera employed to detect the products. However, appearance of the hSOD band at 34 kDa rather than 51 kDa indicates that cleavage occurred.

The P190 expression product appeared only as the full (encoded) length product without cleavage, forming a band at about 40 kDa, which corresponds to the theoretical molecular weight for the uncleaved product. This may indicate that the minimum essential sequence for HCV protease extends to the region between amino acids 199 and 299.

#### Example 6

(Purification of *E. coli* Expressed Protease)

The HCV protease and fragments expressed in Example 5 may be purified as follows:

The bacterial cells in which the polypeptide was expressed are subjected to osmotic shock and mechanical disruption, the insoluble fraction containing the protease is isolated and subjected to differential extraction with an alkaline-NaCl solution, and the polypeptide in the extract purified by chromatography on columns of S-Sepharose® and Q-Sepharose®.

The crude extract resulting from osmotic shock and mechanical disruption is prepared by suspending 1 g of the packed cells in 10 mL of a solution containing 0.02 M Tris HCl, pH 7.5, 10 mM EDTA, 20% sucrose, and incubating for 10 minutes on ice. The cells are then pelleted by centrifugation at 4,000 x g for 15 min at 4°C. After the supernatant is removed, the cell pellets are resuspended in 10 mL of Buffer A1 (0.01 M Tris HCl, pH 7.5, 1 mM EDTA, 14 mM  $\beta$ -mercap-

toethanol - "BME"), and incubated on ice for 10 minutes. The cells are again pelleted at 4,000 x g for 15 minutes at 4°C. After removal of the clear supernatant (periplasmic fraction I), the cell pellets are resuspended in Buffer A1, incubated on ice for 10 minutes, and again centrifuged at 4,000 x g for 15 minutes at 5 4°C. The clear supernatant (periplasmic fraction II) is removed, and the cell pellet resuspended in 5 mL of Buffer T2 (0.02 M Tris HCl, pH 7.5, 14 mM BME, 1 mM EDTA, 1 mM PMSF). In order to disrupt the cells, the suspension (5 mL) and 7.5 mL of Dyno-mill lead-free acid washed glass beads (0.10-0.15 mm diameter) (available from Glen-Mills, Inc.) are placed in a Falcon tube and vortexed at 10 top speed for two minutes, followed by cooling for at least 2 min on ice. The vortexing-cooling procedure is repeated another four times. After vortexing, the slurry is filtered through a sintered glass funnel using low suction, the glass beads washed twice with Buffer A2, and the filtrate and washes combined.

The insoluble fraction of the crude extract is collected by centrifugation at 15 20,000 x g for 15 min at 4°C\*, washed twice with 10 mL Buffer A2, and resuspended in 5 mL of MILLI-Q water.

A fraction containing the HCV protease is isolated from the insoluble material by adding to the suspension NaOH (2 M) and NaCl (2 M) to yield a final concentration of 20 mM each, vortexing the mixture for 1 minute, centrifuging 20 it 20,000 x g for 20 min at 4°C, and retaining the supernatant.

The partially purified protease is then purified by SDS-PAGE. The protease may be identified by western blot, and the band excised from the gel. The protease is then eluted from the band, and analyzed to confirm its amino acid sequence. N-terminal sequences may be analyzed using an automated amino acid 25 sequencer, while C-terminal sequences may be analyzed by automated amino acid sequencing of a series of tryptic fragments.

\*Trademark

Example 7

## (Preparation of Yeast Expression Vector)

(A) P650 (SOD/Protease Fusion)

This vector contains HCV sequence, which includes the wild-type full-length HCV protease coding sequence, fused at the 5' end to a SOD coding sequence. Two fragments, a 441 bp EcoRI/BglII fragment from clone 11b and a 1471 bp BglII/EcoRI fragment from expression vector P500, were used to reconstruct a wild-type, full-length HCV protease coding sequence. These two fragments were ligated together with an EcoRI digested pS356 vector to produce an expression cassette. The expression cassette encodes the ADH2/GAPDH hybrid yeast promoter, human SOD, the HCV protease, and a GAPDH transcription terminator. The resulting vector was digested with BamHI and a 4052 bp fragment was isolated. This fragment was ligated to the BamHI digested pAB24 vector to produce p650. p650 expresses a polypeptide containing, from its amino terminal end, amino acids 1-154 of hSOD, an oligopeptide -Asn-Leu-Gly-Ile-Arg-, and amino acids 819 to 1458 of HCV-1, as shown in Figure 17 of WO 90/11089, published 4 October 1990.

Clone 11b was isolated from the genomic library of HCV cDNA, ATCC accession no. 40394, as described above in Example 3A, using a hybridization probe having the following sequence:

5' CAC CTA TGT TTA TAA CCA TCT CAC TCC TCT 3'.

This procedure is also described in EPO Pub. No. 318 216, Example IV.A.17.

The vector pS3EF, which is a pBR322 derivative, contains the ADH2/GAPDH hybrid yeast promoter upstream of the human superoxide dimutase gene, an adaptor, and a downstream yeast effective transcription terminator. A similar expression vector containing these control elements and the superoxide dismutase gene is described in Cousens et al. (1987) Gene 61: 265, and in copending application EPO 196,056, published October 1, 1986. pS3EF,

- 37 -

however, differs from that in Cousens et al. in that the heterologous proinsulin gene and the immunoglobulin hinge are deleted, and Gln<sub>134</sub> of SOD is followed by an

adaptor sequence which contains an EcoRI site. The sequence of the adaptor is:

5' AAT TTG GGA ATT CCA TAA TTA ATT AAG 3'  
3' AC CCT TAA GGT ATT AAT TAA TTC AGCT 5'

The EcoRI site facilitates the insertion of heterologous sequences. Once inserted into pS3EF, a SOD fusion is expressed which contains an oligopeptide that links SOD to the heterologous sequences. pS3EF is exactly the same as pS356 except that pS356 contains a different adaptor. The sequence of the adaptor is shown below:

5' AAT TTG GGA ATT CCA TAA TGA G 3'  
3' AC CCT TAA GGT ATT ACT CAG CT 5'

pS356, ATCC accession no. 67683, is deposited as set forth below.

Plasmid pAB24 is a yeast shuttle vector, which contains pBR322 sequences, the complete 2 $\mu$  sequence for DNA replication in yeast (Broach (1981) in: Molecular Biology of the Yeast Saccharomyces, Vol. 1, p. 445, Cold spring Harbor Press.) and the yeast LEU<sup>2d</sup> gene derived from plasmid pC1/1, described in EPO Pub. No. 116 201. Plasmid pAB24 was constructed by digesting YEp24 with EcoRI and re-ligating the vector to remove the partial 2 micron sequences. The resulting plasmid, YEp24deltaRI, was linearized with ClaI and ligated with the complete 2 micron plasmid which had been linearized with ClaI. The resulting plasmid, pCBou, was then digested with XbaI, and the 8605 bp vector fragment was gel isolated. This isolated XbaI fragment was ligated with a 4460 bp XbaI fragment containing the LEU<sup>2d</sup> gene isolated from pC1/1; the orientation of LEU<sup>2d</sup> gene is in the same direction as the URA3 gene.

*S. cerevisiae*, 2150-2-3 (pAB24-GAP-env2), accession no. 20827, is deposited with the American Type Culture Collection as set forth below. The plasmid pAB24-GAP-env2 can be recovered from the yeast cells by known

techniques. The GAP-env2 expression cassette can be removed by digesting pAB24-GAP-env2 with BamHI. pAB24 is recovered by religating the vector without the BamHI insert.

5

Example 8

(Yeast Expression of SOD-Protease Fusion Protein)

p650 was transformed in *S. cerevisiae* strain JSC310, Mata, leu2, ura3-52, prb1-1122, pep4-3, prc1-407, cir<sup>+</sup>: DM15 (g418 resistance). The transformation is as described by Hinnen et al. (1978) Proc Natl Acad Sci USA 75: 1929. The transformed cells were selected on ura- plates with 8% glucose. The plates were incubated at 30°C for 4-5 days. The transformants were further selected on leu- plates with 8% glucose putatively for high numbers of the p650 plasmid. Colonies from the leu- plates were inoculated into leu- medium with 3% glucose. These cultures were shaken at 30°C for 2 days and then diluted 1/20 into YEPD medium with 2% glucose and shaken for 2 more days at 30°C.

15

*S. cerevisiae* JSC310 contains DM15 DNA, described in EPO Pub. No. 340 986, published 8 November 1989. This DM15 DNA enhances ADH2 regulated expression of heterologous proteins. pDM15, accession no. 40453, is deposited with the American Type Culture Collection as set forth below.

20

Example 9

(Yeast Ubiquitin Expression of Mature HCV Protease)

Mature HCV protease is prepared by cleaving vector C7fC20cC300C200 with EcoRI to obtain a 2 Kb coding sequence, and inserting the sequence with the appropriate linkers into a ubiquitin expression vector, such as that described in WO 88/02406, published 7 April 1988,

25

Mature HCV protease is recovered upon expression of the vector in suitable hosts, particularly yeast.

- 39 -

Specifically, the yeast expression protocol described in Example 8 is used to express a ubiquitin/HCV protease vector.

#### Example 10

5 (Preparation of an In-Vitro Expression Vector)

(A) pGEM®-3Z/Yellow Fever Leader Vector

Four synthetic DNA fragments were annealed and ligated\*\* together to create a EcoRI/SacI Yellow Fever leader, which was ligated to a EcoRI/SacI digested pGEM®-3Z vector from Promega®. The sequence of the  
10 four fragments are listed below:

YFK-1:

5' AAT TCG TAA ATC CTG TGT GCT AAT TGA GGT GCA TTG GTC  
TGC AAA TCG AGT TGC TAG GCA ATA AAC ACA TT 3'

YFK-2:

15 5' TAT TGC CTA GCA ACT CGA TTT GCA GAC CAA TGC ACC TCA ATT  
AGC ACA CAG GAT TTA CG 3'

YFK-3:

5' TGG ATT AAT TTT AAT CGT TCG TTG AGC GAT TAG CAG AGA  
ACT GAC CAG AAC ATG TCT GAG CT 3'

20 YFK-4:

5' CAG ACA TGT TCT GGT CAG TTC TCT GCT AAT CGC TCA ACG AAC  
GAT TAA AAT TAA TCC AAA TGT GTT 3'.

For in-vitro translation of the HCV protease, the new pGEM®-  
3Z/Yellow Fever leader vector was digested with BamHI and blunted with  
25 Klenow.

(B) PvuII Construct from p6000

A clone p6000 was constructed from sequences available from the genomic library of HCV cDNA, ATCC accession no. 40394. The HCV encoding

- 40 -

DNA sequence of p6000 is identical to nucleotide -275 to nucleotide 6372 of Figure 17 of WO 90/11089, published 4 October 1990. p6000 was digested with PvuII, and from the digest, a 2,864 bp fragment was isolated. This 2,864 bp fragment was ligated to the prepared pGEM®-3Z/Yellow Fever leader vector  
5 fragment, described above.

### Example 11

#### (In-Vitro Expression of HCV Protease)

##### (A) Transcription

10 The pGEM®-3Z/Yellow Fever leader/PvuII vector was linearized with XbaI and transcribed using the materials and protocols from Promega's Riboprobe® Gemini II Core system.

##### (B) Translation

15 The RNA produced by the above protocol was translated using Promega's rabbit reticulocyte lysate, minus methionine, canine pancreatic microsomal membranes, as well as, other necessary materials and instructions from Promega.

#### 20 Deposited Biological Materials:

The following materials were deposited with the American Type Culture Collection (ATCC), 12301 Parklawn Dr., Rockville, Maryland:

	<u>Name</u>	<u>Deposit Date</u>	<u>Accession No.</u>
25	<i>E. coli</i> D1210, cf1SODp600	23 Mar 1990	68275
	Cf1/5-1-1 in <i>E. coli</i> D1210	11 May 1989	67967
30	Bacteriophage λ-gt11 cDNA library	01 Dec 1987	40394

	<i>E. coli</i> HB101, pS356	29 Apr 1988	67683
	plasmid DNA, pDM15	05 May 1988	40453
5	<i>S. cerevisiae</i> , 2150-2-3 (pAB24-GAP-env2)	23 Dec 1986	20827

10 The above materials have been deposited with the ATCC under the accession numbers indicated. These deposits will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided as a convenience to those of skill in the art.

15 The polynucleotide sequences contained in the deposited materials, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the sequences described herein. A license may be required to make, use or sell the deposited materials, and no such license is granted hereby.



**PCT/US91/02210**

1/21

### Figure 1

2079105

2/21

**PCT/US91/02210**

			130					135				140			
Thr	Cys	Ile	Ile	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly
ACG	TGC	ATC	ATC	AAT	GGG	GTG	TGC	TGG	ACT	GTC	TAC	CAC	GGG	GCC	GGA
TGC	ACG	TAG	TAG	TTA	CCC	CAC	ACG	ACC	TGA	CAG	ATG	GTG	CCC	CGG	CCT

		145					150					155			
Thr	Arg	Thr	Ile	Ala	Ser	Pro	Lys	Gly	Pro	Val	Ile	Gln	Met	Tyr	Thr
ACG	AGG	ACC	ATC	GCG	TCA	CCC	AAG	GGT	CCT	GTC	ATC	CAG	ATG	TAT	ACC
TGC	TCC	TGG	TAG	CGC	AGT	GGG	TTC	CCA	GGA	CAG	TAG	GTC	TAC	ATA	TGG

160					165					170					
Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Pro	Ala	Ser	Gln	Gly	Thr	Arg
AAT	GTA	GAC	CAA	GAC	CTT	GTG	GGC	TGG	CCC	GCT	TCG	CAA	GGT	ACC	CGC
TTA	CAT	CTG	GTT	CTG	GAA	CAC	CCG	ACC	GGG	CGA	AGC	GTT	CCA	TGG	GCG

175					180					185					190				
Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr				
TCA	TTG	ACA	CCC	TGC	ACT	TGC	GGC	TCC	TCG	GAC	CTT	TAC	CTG	GTC	ACG				
AGT	AAC	TGT	GGG	ACG	TGA	ACG	CCG	AGG	AGC	CTG	GAA	ATG	GAC	CAG	TGC				

				195					200					205		
Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	
AGG	CAC	GCC	GAT	GTC	ATT	CCC	GTG	CGC	CGG	CGG	GGT	GAT	AGC	AGG	GGC	
TCC	GTG	CGG	CTA	CAG	TAA	GGG	CAC	GCG	GCC	GCC	CCA	CTA	TCG	TCC	CCG	

↑  
**NaeI**

			210					215					220			
Ser	Leu	Leu	Ser	Pro	Arg	Pro	Ile	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	
AGC	CTG	CTG	TCG	CCC	CGG	CCC	ATT	TCC	TAC	TTG	AAA	GGC	TCC	TCG	GGG	
TCG	GAC	GAC	AGC	GGG	GCC	GGG	TAA	AGG	ATG	AAC	TTT	CCG	AGG	AGC	CCC	

225						230					235				
Gly	Pro	Leu	Leu	Cys	Pro	Ala	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala
GGT	CCG	CTG	TTG	TGC	CCC	GCG	GGG	CAC	GCC	GTG	GGC	ATA	TTT	AGG	GCC
CCA	GGC	GAC	AAC	ACG	GGG	CGC	CCC	GTG	CGG	CAC	CCG	TAT	AAA	TCC	CGG

240					245					250					
Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Ile	Pro	Val
GCG	GTG	TGC	ACC	CGT	GGA	GTG	GCT	AAG	GCG	GTG	GAC	TTT	ATC	CCT	GTG
CGC	CAC	ACG	TGG	GCA	CCT	CAC	CGA	TTC	CGC	CAC	CTG	AAA	TAG	GGA	CAC

**Figure 1 (continued)**

2079105

3/21

**PCT/US91/02210**

255					260					265					270
Glu	Asn	Leu	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser
GAG	AAC	CTA	GAG	ACA	ACC	ATG	AGG	TCC	CCG	GTG	TTC	ACG	GAT	AAC	TCC
CTC	TTG	GAT	CTC	TGT	TGG	TAC	TCC	AGG	GGC	CAC	AAG	TGC	CTA	TTG	AGG

275							280							285		
Ser	Pro	Pro	Val	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	
TCT	CCA	CCA	GTA	GTG	CCC	CAG	AGC	TTC	CAG	GTG	GCT	CAC	CTC	CAT	GCT	
AGA	GGT	GGT	CAT	CAC	GGG	GTC	TCG	AAG	GTC	CAC	CGA	GTG	GAG	GTA	CGA	

			290					295					300			
Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	
CCC	ACA	GGC	AGC	GGC	AAA	AGC	ACC	AAG	GTC	CCG	GCT	GCA	TAT	GCA	GCT	
GGG	TGT	CCG	TCG	CCG	TTT	TCG	TGG	TTC	CAG	GGC	CGA	CGT	ATA	CGT	CGA	

**NdeI**

305						310						315					
Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu		
CAG	GGC	TAT	AAG	GTG	CTA	GTA	CTC	AAC	CCC	TCT	GTT	GCT	GCA	ACA	CTG		
GTC	CCG	ATA	TTC	CAC	GAT	CAT	GAG	TTG	GGG	AGA	CAA	CGA	CGT	TGT	GAC		

320						325				330					
Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile
GGC	TTT	GGT	GCT	TAC	ATG	TCC	AAG	GCT	CAT	GGG	ATC	GAT	CCT	AAC	ATC
CCG	AAA	CCA	CGA	ATG	TAC	AGG	TTC	CGA	GTA	CCC	TAG	CTA	GGA	TTG	TAG

335				340				345				350			
Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ser	Pro	Ile	Thr	Tyr	Ser
AGG	ACC	GGG	GTG	AGA	ACA	ATT	ACC	ACT	GGC	AGC	CCC	ATC	ACG	TAC	TCC
TCC	TGG	CCC	CAC	TCT	TGT	TAA	TGG	TGA	CCG	TCG	GGG	TAG	TGC	ATG	AGG

				355					360					365		
Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	
ACC	TAC	GGC	AAG	TTC	CTT	GCC	GAC	GGC	GGG	TGC	TCG	GGG	GGC	GCT	TAT	
TGG	ATG	CCG	TTC	AAG	GAA	CGG	CTG	CCG	CCC	ACG	AGC	CCC	CCG	CGA	ATA	

370					375					380					
Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ala	Thr	Ser	Ile
GAC	ATA	ATA	ATT	TGT	GAC	GAG	TGC	CAC	TCC	ACG	GAT	GCC	ACA	TCC	ATC
CTG	TAT	TAT	TAA	ACA	CTG	CTC	ACG	GTG	AGG	TGC	CTA	CGG	TGT	AGG	TAG

**Figure 1 (continued)**

**PCT/US91/02210**

**WO 91/15575**

4/21

			385				390						395				
Leu	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg		
TTG	GGC	ATT	GGC	ACT	GTC	CTT	GAC	CAA	GCA	GAG	ACT	GCG	GGG	GCG	AGA		
AAC	CCG	TAA	CCG	TGA	CAG	GAA	CTG	GTT	CGT	CTC	TGA	CGC	CCC	CGC	TCT		

400						405				410					
Leu	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro
CTG	GTT	GTG	CTC	GCC	ACC	GCC	ACC	CCT	CCG	GGC	TCC	GTC	ACT	GTG	CCC
GAC	CAA	CAC	GAG	CGG	TGG	CGG	TGG	GGA	GGC	CCG	AGG	CAG	TGA	CAC	GGG

<b>415</b>					<b>420</b>					<b>425</b>					<b>430</b>
<b>His</b>	<b>Pro</b>	<b>Asn</b>	<b>Ile</b>	<b>Glu</b>	<b>Glu</b>	<b>Val</b>	<b>Ala</b>	<b>Leu</b>	<b>Ser</b>	<b>Thr</b>	<b>Thr</b>	<b>Gly</b>	<b>Glu</b>	<b>Ile</b>	<b>Pro</b>
<b>CAT</b>	<b>CCC</b>	<b>AAC</b>	<b>ATC</b>	<b>GAG</b>	<b>GAG</b>	<b>GTT</b>	<b>GCT</b>	<b>CTG</b>	<b>TCC</b>	<b>ACC</b>	<b>ACC</b>	<b>GGA</b>	<b>GAG</b>	<b>ATC</b>	<b>CCT</b>
<b>GTA</b>	<b>GGG</b>	<b>TTG</b>	<b>TAG</b>	<b>CTC</b>	<b>CTC</b>	<b>CAA</b>	<b>CGA</b>	<b>GAC</b>	<b>AGG</b>	<b>TGG</b>	<b>TGG</b>	<b>CCT</b>	<b>CTC</b>	<b>TAG</b>	<b>GGA</b>

				435					440					445		
Phe	Tyr	Gly	Lys	Ala	Ile	Pro	Leu	Glu	Val	Ile	Lys	Gly	Gly	Arg	His	
TTT	TAC	GGC	AAG	GCT	ATC	CCC	CTC	GAA	GTA	ATC	AAG	GGG	GGG	AGA	CAT	
AAA	ATG	CCG	TTC	CGA	TAG	GGG	GAG	CTT	CAT	TAG	TTC	CCC	CCC	TCT	GTA	

			450					455					460			
Leu	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	
CTC	ATC	TTC	TGT	CAT	TCA	AAG	AAG	AAG	TGC	GAC	GAA	CTC	GCC	GCA	AAG	
GAG	TAG	AAG	ACA	GTA	AGT	TTC	TTC	TTC	ACG	CTG	CTT	GAG	CGG	CGT	TTC	

465							470				475				
Leu	Val	Ala	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp
CTG	GTC	GCA	TTG	GGC	ATC	AAT	GCC	GTG	GCC	TAC	TAC	CGC	GGT	CTT	GAC
GAC	CAG	CGT	AAC	CCG	TAG	TTA	CGG	CAC	CGG	ATG	ATG	GCG	CCA	GAA	CTG

480						485				490							
Val	Ser	Val	Ile	Pro	Thr	Ser	Gly	Asp	Val	Val	Val	Val	Val	Ala	Thr	Asp	
GTG	TCC	GTC	ATC	CCG	ACC	AGC	GGC	GAT	GTT	GTC	GTC	GTG	GCA	ACC	GAT		
CAC	AGG	CAG	TAG	GGC	TGG	TCG	CCG	CTA	CAA	CAG	CAG	CAC	CGT	TGG	CTA		

**Figure 1 (continued)**

2079105

WO 91/15575

5/21

PCT/US91/02210

495 500 505 510  
 Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys  
 GCC CTC ATG ACC GGC TAT ACC GGC GAC TTC GAC TCG GTG ATA GAC TGC  
 CGG GAG TAC TGG CCG ATA TGG CCG CTG AAG CTG AGC CAC TAT CTG ACC

515 520 525  
 Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe  
 AAT ACG TGT GTC ACC CAG ACA GTC GAT TTC AGC CTT GAC CCT ACC TTC  
 TTA TGC ACA CAG TGG GTC TGT CAG CTA AAG TCG GAA CTG GGA TGG AAG

530 535 540  
 Thr Ile Glu Thr Ile Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln  
 ACC ATT GAG ACA ATC ACG CTC CCC CAA GAT GCT GTC TCC CGC ACT CAA  
 TGG TAA CTC TGT TAG TGC GAG GGG GTT CTA CGA CAG AGG GCG TGA GTT

545 550 555  
 Arg Arg Gly Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val  
 CGT CGG GGC AGG ACT GGC AGG GGG AAG CCA GGC ATC TAC AGA TTT GTG  
 GCA GCC CCG TCC TGA CCG TCC CCC TTC GGT CCG TAG ATG TCT AAA CAC

560 565 570  
 Ala Pro Gly Glu Arg Pro Pro Gly Met Phe Asp Ser Ser Val Leu Cys  
 GCA CCG GGG GAG CGC CCT CCC GGC ATG TTC GAC TCG TCC GTC CTC TGT  
 CGT GGC CCC CTC GCG GGA GGG CCG TAC AAG CTG AGC AGG CAG GAG ACA

575 580 585 590  
 Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu  
 GAG TGC TAT GAC GCA GGC TGT GCT TGG TAT GAG CTC ACG CCC GCC GAG  
 CTC ACG ATA CTG CGT CCG ACA CGA ACC ATA CTC GAG TGC GGG CCG CTC

595 600 605  
 Thr Thr Val Arg Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu Pro Val  
 ACT ACA GTT AGG CTA CGA GCG TAC ATG AAC ACC CCG GGG CTT CCC GTG  
 TGA TGT CAA TCC GAT GCT CGC ATG TAC TTG TGG GGC CCC GAA GGG CAC

Figure 1 (continued)

2079105

			610					615					620				
Cys	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Gly	Val	Phe	Thr	Gly	Leu	Thr		
TGC	CAG	GAC	CAT	CTT	GAA	TTT	TGG	GAG	GGC	GTC	TTT	ACA	GGC	CTC	ACT		
ACG	GTC	CTG	GTA	GAA	CTT	AAA	ACC	CTC	CCG	CAG	AAA	TGT	CCG	GAG	TGA		

		625						630					635				
His	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ser	Gly	Glu	Asn		
CAT	ATA	GAT	GCC	CAC	TTT	CTA	TCC	CAG	ACA	AAG	CAG	AGT	GGG	GAG	AAC		
GTA	TAT	CTA	CGG	GTG	AAA	GAT	AGG	GTC	TGT	TTC	GTC	TCA	CCC	CTC	TTG		

		640						645					650				
Leu	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln		
CTT	CCT	TAC	CTG	GTA	GCG	TAC	CAA	GCC	ACC	GTG	TGC	GCT	AGG	GCT	CAA		
GAA	GGA	ATG	GAC	CAT	CGC	ATG	GTT	CGG	TGG	CAC	ACG	CGA	TCC	CGA	GTT		

								660					665				670
Ala	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu		
GCC	CCT	CCC	CCA	TCG	TGG	GAC	CAG	ATG	TGG	AAG	TGT	TTG	ATT	CGC	CTC		
CGG	GGA	GGG	GGT	AGC	ACC	CTG	GTC	TAC	ACC	TTC	ACA	AAC	TAA	GCG	GAG		

								675									685
Lys	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala		
AAG	CCC	ACC	CTC	CAT	GGG	CCA	ACA	CCC	CTG	CTA	TAC	AGA	CTG	GGC	GCT		
TTC	GGG	TGG	GAG	GTA	CCC	GGT	TGT	GGG	GAC	GAT	ATG	TCT	GAC	CCG	CGA		

Figure 1

B

2079105

WO 91/15575

PCT/US91/02210

C20G:

7/21

Asn Ser Glu Asn Gln Val Glu Gly Glu Val Gln Ile Val Ser Thr Ala  
 AAT TCG GAA AAC CAA GTG GAG GGT GAG GTC CAG ATT GTG TCA ACT GCT  
 TTA AGC CTT TTG GTT CAC CTC CCA CTC CAG GTC TAA CAC AGT TGA CGA  
 ↑  
 EcoRI

Ala Gln Thr Phe Leu Ala Thr Cys Ile Asn Gly Val Cys Trp Thr Val  
 GCC CAA ACC TTC CTG GCA ACG TGC ATC AAT GGG GTG TGC TGG ACT GTC  
 CGG GTT TGG AAG GAC CGT TGC ACG TAG TTA CCC CAC ACG ACC TGA CAG  
 ↑  
 SfaNI

Tyr His Gly Ala Gly Thr Arg Thr Ile Ala Ser Pro Lys Gly Pro Val  
 TAC CAC GGG GCC GGA ACG AGG ACC ATC GCG TCA CCC AAG GGT CCT GTC  
 ATG GTG CCC CGG CCT TGC TCC TGG TAG CGC AGT GGG TTC CCA GGA CAG

Ile Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Pro Ala  
 ATC CAG ATG TAT ACC AAT GTA GAC CAA GAC CTT GTG GGC TGG CCC GCT  
 TAG GTC TAC ATA TGG TTA CAT CTG GTT CTG GAA CAC CCG ACC GGG CGA

Ser Gln Gly Thr Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp  
 TCG CAA GGT ACC CGC TCA TTG ACA CCC TGC ACT TGC GGC TCC TCG GAC  
 AGC GTT CCA TGG GCG AGT AAC TGT GGG ACG TGA ACG CCG AGG AGC CTG

Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg  
 CTT TAC CTG GTC ACG AGG CAC GCC GAT GTC ATT CCC GTG CGC CGG CGG  
 GAA ATG GAC CAG TGC TCC GTG CGG CTA CAG TAA GGG CAC GCG GCC GCC  
 ↑  
 NaeI

Gly Asp Ser Arg Gly Ser Leu Val Ser Pro Arg Pro Ile Ser Tyr Leu  
 GGT GAT AGC AGG GGC AGC CTC GTG TCG CCC CGG CCC ATT TCC TAC TTG  
 CCA CTA TCG TCC CCG TCG GAG CAC AGC GGG GCC GGG TAA AGG ATG AAC

Lys Gly Ser Ser Gly Gly Pro Leu Pro Asn  
 AAA GGC TCC TCG GGG GGT CCG CTG CCG AAT TC  
 TTT CCG AGG AGC CCC CCA GGC GAC GGC TTA AG  
 ↑  
 EcoRI

Figure 2

WO 91/15575

2079105

PCT/US91/02210

8/21

C26d:

Glu Phe Gly Gly Leu Leu Leu Cys Pro Ala Ala Ala Val Gly Ile Phe  
GAA TTC GGG GGC CTG CTG TTG TGC CCC GCG GCA GCC GTG GGC ATA TTT  
CTT AAG CCC CCG GAC GAC AAC ACG GGG CGC CGT CGG CAC CCG TAT AAA  
↑  
EcoRI

Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile  
AGG GCC GCG GTG TGC ACC CGT GGA GTG GCT AAG GCG GTG GAC TTT ATC  
TCC CGG CGC CAC ACG TGG GCA CCT CAC CGA TTC CGC CAC CTG AAA TAG  
↑  
DdeI

Pro Val Glu Asn Leu Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp  
CCT GTG GAG AAC CTA GAG ACA ACC ATG AGG TCC CCG GTG TTC ACG GAT  
GGA CAC CTC TTG GAT CTC TGT TGG TAC TCC AGG GGC CAC AAG TGC CTA

Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val Ala His Leu  
AAC TCC TCT CCA CCA GTA GTG CCC CAG AGC TTC CAG GTG GCT CAC CTC  
TTG AGG AGA GGT GGT CAT CAC GGG GTC TCG AAG GTC CAC CGA GTG GAG  
↑  
EcoRII

His Ala Pro Arg Ile  
CAT GCT CCC CGA ATT C  
GTA CGA GGG GCT TAA G  
↑  
EcoRI

Figure 3



WO 91/15575

2079105

PCT/US91/02210

9/21

C8h:

Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala  
CCC TGC ACT TGC GGC TCC TCG GAC CTT TAC CTG GTC ACG AGG CAC GCC  
GGG ACG TGA ACG CCG AGG AGC CTG GAA ATG GAC CAG TGC TCC GTG CGG

Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu  
GAT GTC ATT CCC GTG CGC CGG CGG GGT GAT AGC AGG GGC AGC CTG CTG  
CTA CAG TAA GGG CAC GCG GCC GCC CCA CTA TCG TCC CCG TCG GAC GAC

Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu  
TCG CCC CGG CCC ATT TCC TAC TTG AAA GGC TCC TCG GGG GGT CCG CTG  
AGC GGG GCC GGG TAA AGG ATG AAC TTT CCG AGG AGC CCC CCA GGC GAC

Leu Cys Pro Ala Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys  
TTG TGC CCC GCG GGG CAC GCC GTG GGC ATA TTT AGG GCC GCG GTG TGC  
AAC ACG GGG CCG CCC GTG CGG CAC CCG TAT AAA TCC CGG CCG CAC ACG

Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Asn Leu  
ACC CGT GGA GTG GCT AAG GCG GTG GAC TTT ATC CCT GTG GAG AAC CTA  
TGG GCA CCT CAC CGA TTC CGC CAC CTG AAA TAG GGA CAC CTC TTG GAT

↑  
DdeI

Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser  
GAG ACA ACC ATG AGG TCC CCG GTG TTC ACG GAT AAC TCC TC  
CTC TGT TGG TAC TCC AGG GGC CAC AAG TGC CTA TTG AGG AG

Figure 4

**PCT/US91/02210**

10/21

Ile Arg Gly Thr Tyr Val Tyr Asn His Leu Thr Pro Leu Arg Asp Trp  
ATT CGG GGC ACC TAT GTT TAT AAC CAT CTC ACT CCT CTT CGG GAC TGG  
TAA GCC CCG TGG ATA CAA ATA TTG GTA GAG TGA GGA GAA GCC CTG ACC  
↑  
EcoRI

<b>Ala</b>	<b>His</b>	<b>Asn</b>	<b>Gly</b>	<b>Leu</b>	<b>Arg</b>	<b>Asp</b>	<b>Leu</b>	<b>Ala</b>	<b>Val</b>	<b>Ala</b>	<b>Val</b>	<b>Glu</b>	<b>Pro</b>	<b>Val</b>	<b>Val</b>
<b>GCG</b>	<b>CAC</b>	<b>AAC</b>	<b>GGC</b>	<b>TTG</b>	<b>CGA</b>	<b>GAT</b>	<b>CTG</b>	<b>GCC</b>	<b>GTG</b>	<b>GCT</b>	<b>GTA</b>	<b>GAG</b>	<b>CCA</b>	<b>GTC</b>	<b>GTC</b>
<b>CGC</b>	<b>GTG</b>	<b>TTG</b>	<b>CCG</b>	<b>AAC</b>	<b>GCT</b>	<b>CTA</b>	<b>GAC</b>	<b>CGG</b>	<b>CAC</b>	<b>CGA</b>	<b>CAT</b>	<b>CTC</b>	<b>GGT</b>	<b>CAG</b>	<b>CAG</b>

**Phe Ser Gln Met Glu Thr Lys Leu Ile Thr Trp Gly Ala Asp Thr Ala**  
**TTC TCC CAA ATG GAG ACC AAG CTC ATC ACG TGG GGG GCA GAT ACC GCC**  
**AAG AGG GTT TAC CTC TGG TTC GAG TAG TGC ACC CCC CGT CTA TGG CGG**

**Ala Cys Gly Asp Ile Ile Asn Gly Leu Pro Val Ser Ala Arg Arg Gly**  
**GCG TGC GGT GAC ATC ATC AAC GGC TTG CCT GTT TCC GCC CGC AGG GGC**  
**CGC ACG CCA CTG TAG TAG TTG CCG AAC GGA CAA AGG CGG GCG TCC CCG**

Arg Glu Ile Leu Leu Gly Pro Ala Asp Gly Met Val Ser Lys Gly Trp  
CGG GAG ATA CTG CTC GGG CCA GCC GAT GGA ATG GTC TCC AAG GGT TGG  
GCC CTC TAT GAC GAG CCC GGT CGG CTA CCT TAC CAG AGG TTC CCA ACC

Arg	Leu	Leu	Ala	Pro	Ile	Thr	Ala	Tyr	Ala	Gln	Gln	Thr	Arg	Gly	Leu
AGG	TTG	CTG	GCG	CCC	ATC	ACG	GCG	TAC	GCC	CAG	CAG	ACA	AGG	GGC	CTC
TCC	AAC	GAC	CGC	GGG	TAG	TGC	CGC	ATG	CGG	GTC	GTC	TGT	TCC	CCG	GAG

Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
CTA GGG TGC ATA ATC ACC AGC CTA ACT GGC CGG GAC AAA AAC CAA GTG  
GAT CCC ACG TAT TAG TGG TCG GAT TGA CCG GCC CTG TTT TTG GTT CAC

**Glu Gly Glu Val Gln Ile Val Ser Thr Ala Ala Gln Thr Phe Leu Ala**  
**GAG GGT GAG GTC CAG ATT GTG TCA ACT GCT GCC CAA ACC TTC CTG GCA**  
**CTC CCA CTC CAG GTC TAA CAC AGT TGA CGA CGG GTT TGG AAG GAC CGT**

Thr	Cys	Ile	Asn	Gly	Val	Cys	Trp	Pro	Asn
ACG	TGC	ATC	AAT	GGG	GTG	TGC	TGG	CCG	AAT
TGC	ACG	TAG	TTA	CCC	CAC	ACG	ACC	GGC	TTA
		↑							↑
		SfaNI							EcoRI

### Figure 5

C31:

Glu Phe Gly Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ala  
 GAA TTC GGG TCC GTC ATC CCG ACC AGC GGC GAT GTT GTC GTC GTC GCA  
 CTT AAG CCC AGG CAG TAG GGC TGG TCG CCG CTA CAA CAG CAG CAG CGT

↑  
 EcoRI

Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile  
 ACC GAT GCC CTC ATG ACC GGC TAT ACC GGC GAC TTC GAC TCG GTG ATA  
 TGG CTA CGG GAG TAC TGG CCG ATA TGG CCG CTG AAG CTG AGC CAC TAT

↑  
 HinfI

Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro  
 GAC TGC AAT ACG TGT GTC ACC CAG ACA GTC GAT TTC AGC CTT GAC CCT  
 CTG ACG TTA TGC ACA CAG TGG GTC TGT CAG CTA AAG TCG GAA CTG GGA

Thr Phe Thr Ile Glu Thr Ile Thr Leu Pro Gln Asp Ala Val Ser Arg  
 ACC TTC ACC ATT GAG ACA ATC ACG CTC CCC CAA GAT GCT GTC TCC CGC  
 TGG AAG TGG TAA CTC TGT TAG TGC GAG GGG GTT CTA CGA CAG AGG GCG

Thr Gln Arg Arg Gly Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg  
 ACT CAA CGT CGG GGC AGG ACT GGC AGG GGG AAG CCA GGC ATC TAC AGA  
 TGA GTT GCA GCC CCG TCC TGA CCG TCC CCC TTC GGT CCG TAG ATG TCT

Phe Val Ala Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val  
 TTT GTG GCA CCG GGG GAG CGC CCC TCC GGC ATG TTC GAC TCG TCC GTC  
 AAA CAC CGT GGC CCC CTC GCG GGG AGG CCG TAC AAG CTG AGC AGG CAG

↑  
 BglI

↑  
 HinfI

Leu Cys Glu Cys Pro Asn  
 CTC TGT GAG TGC CCG AAT TC  
 GAG ACA CTC ACG GGC TTA AG

↑  
 EcoRI

Figure 6

C15:

Ile Arg Ser Ile Glu Thr Ile Thr Leu Pro Gln Asp Ala Val Ser Arg  
 ATT CGG TCC ATT GAG ACA ATC ACG CTC CCC CAG GAT GCT GTC TCC CGC  
 TAA GCC AGG TAA CTC TGT TAG TGC GAG GGG GTC CTA CGA CAG AGG GCG

↑  
 EcoRI

Thr Gln Arg Arg Gly Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg  
 ACT CAA CGT CGG GGC AGG ACT GGC AGG GGG AAG CCA GGC ATC TAC AGA  
 TGA GTT GCA GCC CCG TCC TGA CCG TCC CCC TTC GGT CCG TAG ATG TCT

Phe Val Ala Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val  
 TTT GTG GCA CCG GGG GAG CGC CCC TCC GGC ATG TTC GAC TCG TCC GTC  
 AAA CAC CGT GGC CCC CTC GCG GGG AGG CCG TAC AAG CTG AGC AGG CAG

↑  
 BglI

Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro  
 CTC TGT GAG TGC TAT GAC GCA GGC TGT GCT TGG TAT GAG CTC ACG CCC  
 GAG ACA CTC ACG ATA CTG CGT CCG ACA CGA ACC ATA CTC GAG TGC GGG

Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu  
 GCC GAG ACT ACA GTT AGG CTA CGA GCG TAC ATG AAC ACC CCG GGG CTT  
 CGG CTC TGA TGT CAA TCC GAT GCT CGC ATG TAC TTG TGG GGC CCC GAA

Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly  
 CCC GTG TGC CAG GAC CAT CTT GAA TTT TGG GAG GGC GTC TTT ACA GGC  
 GGG CAC ACG GTC CTG GTA GAA CTT AAA ACC CTC CCG CAG AAA TGT CCG

Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ser Gly  
 CTC ACT CAT ATA GAT GCC CAC TTT CTA TCC CAG ACA AAG CAG AGT GGG  
 GAG TGA GTA TAT CTA CGG GTG AAA GAT AGG GTC TGT TTC GTC TCA CCC

Glu Asn Leu Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg  
 GAG AAC CTT CCT TAC CTG GTA GCG TAC CAA GCC ACC GTG TGC GCT AGG  
 CTC TTG GAA GGA ATG GAC CAT CGC ATG GTT CCG TGG CAC ACG CGA TCC

Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile  
 GCT CAA GCC CCT CCC CCA TCG TGG GAC CAG ATG TGG AAG TGT TTG ATT  
 CGA GTT CCG GGA GGG GGT AGC ACC CTG GTC TAC ACC TTC ACA AAC TAA

Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu  
 CGC CTC AAG CCC ACC CTC CAT GGG CCA ACA CCC CTG CTA TAC AGA CTG  
 GCG GAG TTC GGG TGG GAG GTA CCC GGT TGT GGG GAC GAT ATG TCT GAC

Gly Ala Ala Glu Phe  
 GGC GCT GCC GAA TTC  
 CCG CGA CGG CTT AAG

↑  
 EcoRI

Figure 7

2079105

WO 91/15575

PCT/US91/02210

13/21

C33c:

Glu Phe Gly Ala Val Asp Phe Ile Pro Val Glu Asn Leu Glu Thr Thr  
 GAA TTC GGG GCG GTG GAC TTT ATC CCT GTG GAG AAC CTA GAG ACA ACC  
 CTT AAG CCC CGC CAC CTG AAA TAG GGA CAC CTC TTG GAT CTC TGT TGG

↑  
 EcoRI

Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro  
 ATG AGG TCC CCG GTG TTC ACG GAT AAC TCC TCT CCA CCA GTA GTG CCC  
 TAC TCC AGG GGC CAC AAG TGC CTA TTG AGG AGA GGT GGT CAT CAC GGG

Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly Lys  
 CAG AGC TTC CAG GTG GCT CAC CTC CAT GCT CCC ACA GGC AGC GGC AAA  
 GTC TCG AAG GTC CAC CGA GTG GAG GTA CGA GGG TGT CCG TCG CCG TTT

Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu  
 AGC ACC AAG GTC CCG GCT GCA TAT GCA GCT CAG GGC TAT AAG GTG CTA  
 TCG TGG TTC CAG GGC CGA CGT ATA CGT CGA GTC CCG ATA TTC CAC GAT

Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met  
 GTA CTC AAC CCC TCT GTT GCT GCA ACA CTG GGC TTT GGT GCT TAC ATG  
 CAT GAG TTG GGG AGA CAA CGA CGT TGT GAC CCG AAA CCA CGA ATG TAC

Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr  
 TCC AAG GCT CAT GGG ATC GAT CCT AAC ATC AGG ACC GGG GTG AGA ACA  
 AGG TTC CGA GTA CCC TAG CTA GGA TTG TAG TCC TGG CCC CAC TCT TGT

Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu  
 ATT ACC ACT GGC AGC CCC ATC ACG TAC TCC ACC TAC GGC AAG TTC CTT  
 TAA TGG TGA CCG TCG GGG TAG TGC ATG AGG TGG ATG CCG TTC AAG GAA

Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp  
 GCC GAC GGC GGG TGC TCG GGG GGC GCT TAT GAC ATA ATA ATT TGT GAC  
 CGG CTG CCG CCC ACG AGC CCC CCG CGA ATA CTG TAT TAT TAA ACA CTG

Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val  
 GAG TGC CAC TCC ACG GAT GCC ACA TCC ATC TTG GGC ATT GGC ACT GTC  
 CTC ACG GTG AGG TGC CTA CGG TGT AGG TAG AAC CCG TAA CCG TGA CAG

Figure 8

2079105

WO 91/15575

PCT/US91/02210

14/21

Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr  
 CTT GAC CAA GCA GAG ACT GCG GGG GCG AGA CTG GTT GTG CTC GCC ACC  
 GAA CTG GTT CGT CTC TGA CGC CCC CGC TCT GAC CAA CAC GAG CGG TGG

Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu  
 GCC ACC CCT CCG GGC TCC GTC ACT GTG CCC CAT CCC AAC ATC GAG GAG  
 CGG TGG GGA GGC CCG AGG CAG TGA CAC GGG GTA GGG TTG TAG CTC CTC

Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile  
 GTT GCT CTG TCC ACC ACC GGA GAG ATC CCT TTT TAC GGC AAG GCT ATC  
 CAA CGA GAC AGG TGG TGG CCT CTC TAG GGA AAA ATG CCG TTC CGA TAG

Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser  
 CCC CTC GAA GTA ATC AAG GGG GGG AGA CAT CTC ATC TTC TGT CAT TCA  
 GGG GAG CTT CAT TAG TTC CCC CCC TCT GTA GAG TAG AAG ACA GTA AGT

Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile  
 AAG AAG AAG TGC GAC GAA CTC GCC GCA AAG CTG GTC GCA TTG GGC ATC  
 TTC TTC TTC ACG CTG CTT GAG CGG CGT TTC GAC CAG CGT AAC CCG TAG

Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr  
 AAT GCC GTG GCC TAC TAC CGC GGT CTT GAC GTG TCC GTC ATC CCG ACC  
 TTA CGG CAC CGG ATG ATG GCG CCA GAA CTG CAC AGG CAG TAG GGC TGG

Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr  
 AGC GGC GAT GTT GTC GTC GTG GCA ACC GAT GCC CTC ATG ACC GGC TAT  
 TCG CCG CTA CAA CAG CAG CAC CGT TGG CTA CGG GAG TAC TGG CCG ATA

Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Ala Glu Phe  
 ACC GGC GAC TTC GAC TCG GTG ATA GAC TGC AAT ACG TGT GCC GAA TTC  
 TGG CCG CTG AAG CTG AGC CAC TAT CTG ACG TTA TGC ACA CGG CTT AAG

↑  
 HinfI

↑  
 EcoRI

Figure 8 (Continued)

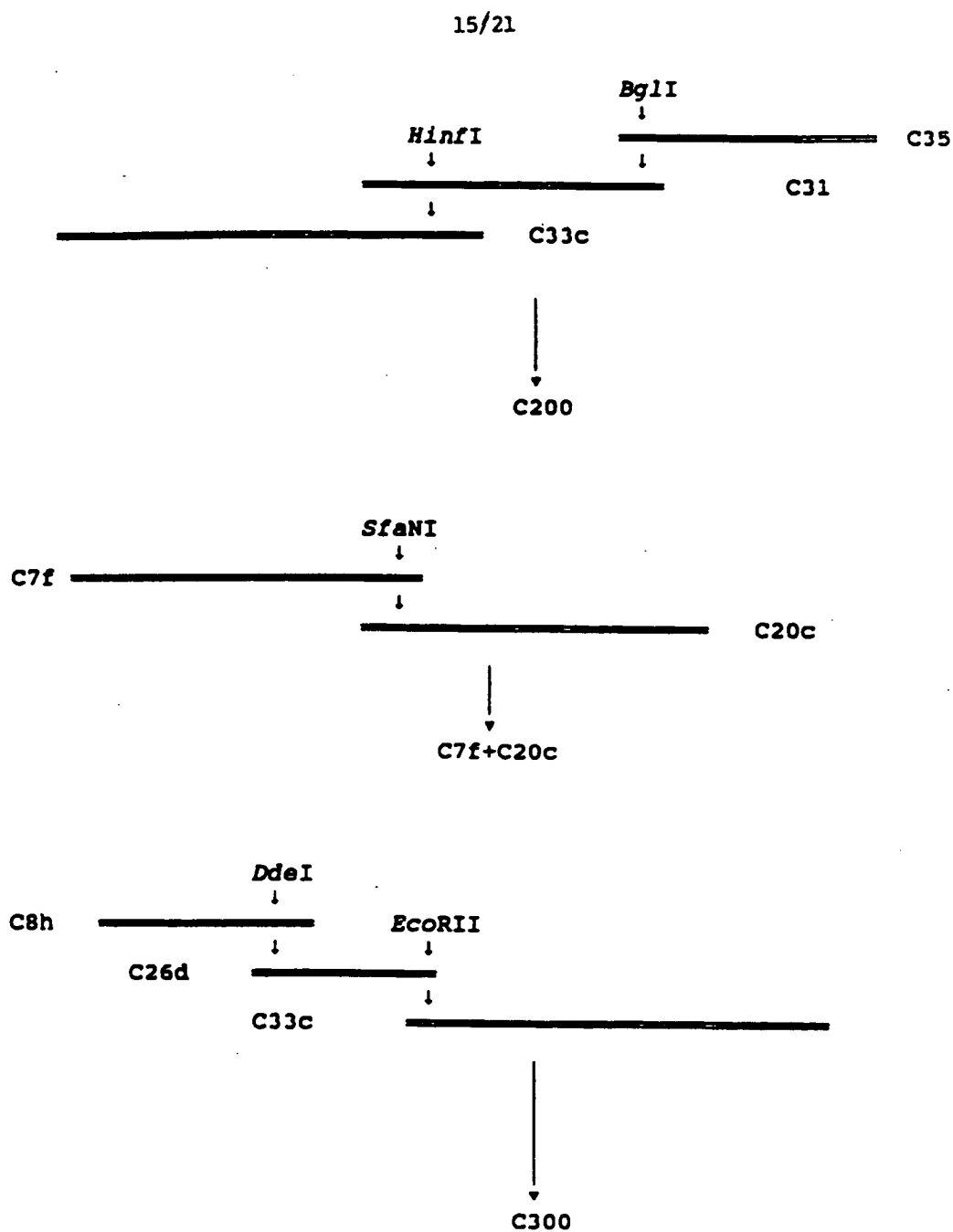


Figure 9

16/21

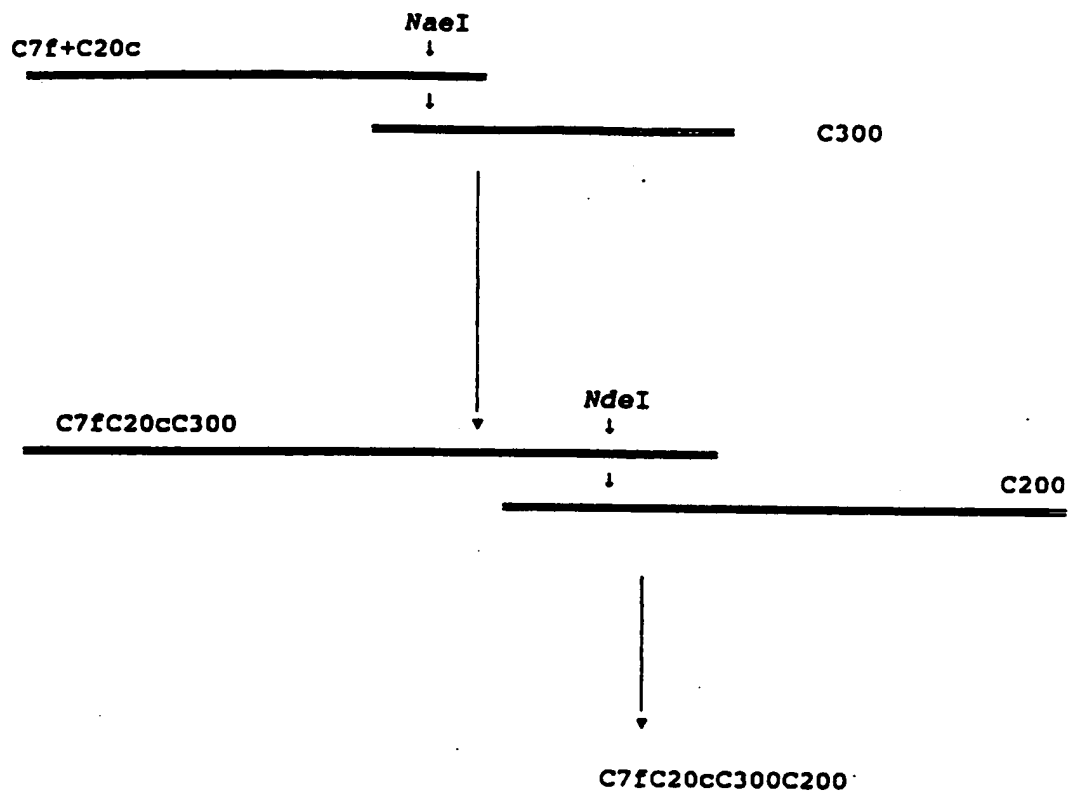


Figure 9 (Continued)



**Figure 10**

18/21

		1				5						10					
Arg	Ile	Gly	Thr	Tyr	Val	Tyr	Asn	His	Leu	Thr	Pro	Leu	Arg	Asp	Trp		
ATT	CGG	GGC	ACC	TAT	GTT	TAT	AAC	CAT	CTC	ACT	CCT	CTT	CGG	GAC	TGG		
TAA	GCC	CCG	TGG	ATA	CAA	ATA	TTG	GTA	GAG	TGA	GGA	GAA	GCC	CTG	ACC		

15					20					25					30
Ala	His	Asn	Gly	Leu	Arg	Asp	Leu	Ala	Val	Ala	Val	Glu	Pro	Val	Val
GCG	CAC	AAC	GGC	TTG	CGA	GAT	CTG	GCC	GTG	GCT	GTA	GAG	CCA	GTC	GTC
CGC	GTG	TTG	CCG	AAC	GCT	CTA	GAC	CGG	CAC	CGA	CAT	CTC	GGT	CAG	CAG

				35					40					45		
Phe	Ser	Gln	Met	Glu	Thr	Lys	Leu	Ile	Thr	Trp	Gly	Ala	Asp	Thr	Ala	
TTC	TCC	CAA	ATG	GAG	ACC	AAG	CTC	ATC	ACG	TGG	GGG	GCA	GAT	ACC	GCC	
AAG	AGG	GTT	TAC	CTC	TGG	TTC	GAG	TAG	TGC	ACC	CCC	CGT	CTA	TGG	CGG	

50					55					60					
Ala	Cys	Gly	Asp	Ile	Ile	Asn	Gly	Leu	Pro	Val	Ser	Ala	Arg	Arg	Gly
GCG	TGC	GGT	GAC	ATC	ATC	AAC	GGC	TTG	CCT	GTT	TCC	GCC	CGC	AGG	GGC
CGC	ACG	CCA	CTG	TAG	TAG	TTG	CCG	AAC	GGA	CAA	AGG	CGG	GCG	TCC	CCG

		65					70					75					
Arg	Glu	Ile	Leu	Leu	Gly	Pro	Ala	Asp	Gly	Met	Val	Ser	Lys	Gly	Trp		
CGG	GAG	ATA	CTG	CTC	GGG	CCA	GCC	GAT	GGA	ATG	GTC	TCC	AAG	GGT	TGG		
GCC	CTC	TAT	GAC	GAG	CCC	GGT	CGG	CTA	CCT	TAC	CAG	AGG	TTC	CCA	ACC		

80					85					90					
Arg	Leu	Leu	Ala	Pro	Ile	Thr	Ala	Tyr	Ala	Gln	Gln	Thr	Arg	Gly	Leu
AGG	TTG	CTG	GCG	CCC	ATC	ACG	GCG	TAC	GCC	CAG	CAG	ACA	AGG	GGC	CTC
TCC	AAC	GAC	CGC	GGG	TAG	TGC	CGC	ATG	CGG	GTC	GTC	TGT	TCC	CCG	GAG

95					100					105					110
Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val
CTA	GGG	TGC	ATA	ATC	ACC	AGC	CTA	ACT	GGC	CGG	GAC	AAA	AAC	CAA	GTG
GAT	CCC	ACG	TAT	TAG	TGG	TCG	GAT	TGA	CCG	GCC	CTG	TTT	TTG	GTT	CAC

				115					120					125			
Glu	Gly	Glu	Val	Gln	Ile	Val	Ser	Thr	Ala	Ala	Gln	Thr	Phe	Leu	Ala		
GAG	GGT	GAG	GTC	CAG	ATT	GTG	TCA	ACT	GCT	GCC	CAA	ACC	TTC	CTG	GCA		
CTC	CCA	CTC	CAG	GTC	TAA	CAC	AGT	TGA	CGA	CGG	GTT	TGG	AAG	GAC	CGT		

**Figure 10 (continued)**

**PCT/US91/02210**

**Figure 10 (continued)**

2079105

WO 91/15575

20/21

PCT/US91/02210

255						260						265				270
Glu	Asn	Leu	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	
GAG	AAC	CTA	GAG	ACA	ACC	ATG	AGG	TCC	CCG	GTG	TTC	ACG	GAT	AAC	TCC	
CTC	TGT	GAT	CTC	TGT	TGG	TAC	TCC	AGG	GGC	CAC	AAG	TGC	CTA	TGT	AGG	

					275						280					285
Ser	Pro	Pro	Val	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	
TCT	CCA	CCA	GTA	GTG	CCC	CAG	AGC	TTC	CAG	GTG	GCT	CAC	CTC	CAT	GCT	
AGA	GGT	GGT	CAT	CAC	GGG	GTC	TCG	AAG	GTC	CAC	CGA	GTG	GAG	GTA	CGA	

					290						295					300
Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	
CCC	ACA	GGC	AGC	GGC	AAA	AGC	ACC	AAG	GTC	CCG	GCT	GCA	TAT	GCA	GCT	
GGG	TGT	CCG	TCG	CCG	TTT	TCG	TGG	TTC	CAG	GGC	CGA	CGT	ATA	CGT	CGA	
													↑			
													NdeI			

					305											
Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	
CAG	GGC	TAT	AAG	GTG	CTA	GTA	CTC	AAC	CCC	TCT	GTT	GCT	GCA	ACA	CTG	
GTC	CCG	ATA	TTC	CAC	GAT	CAT	GAG	TTG	GGG	AGA	CAA	CGA	CGT	TGT	GAC	

					320											
Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	
GGC	TTT	GGT	GCT	TAC	ATG	TCC	AAG	GCT	CAT	GGG	ATC	GAT	CCT	AAC	ATC	
CCG	AAA	CCA	CGA	ATG	TAC	AGG	TTC	CGA	GTA	CCC	TAG	CTA	GGA	TTG	TAG	

335					340						345					350
Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ser	Pro	Ile	Thr	Tyr	Ser	
AGG	ACC	GGG	GTG	AGA	ACA	ATT	ACC	ACT	GGC	AGC	CCC	ATC	ACG	TAC	TCC	
TCC	TGG	CCC	CAC	TCT	TGT	TAA	TGG	TGA	CCG	TCG	GGG	TAG	TGC	ATG	AGG	

					355						360					365
Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	
ACC	TAC	GGC	AAG	TTC	CTT	GCC	GAC	GGC	GGG	TGC	TCG	GGG	GGC	GCT	TAT	
TGG	ATG	CCG	TTC	AAG	GAA	CGG	CTG	CCG	CCC	ACG	AGC	CCC	CCG	CGA	ATA	

					370											
Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ala	Thr	Ser	Ile	
GAC	ATA	ATA	ATT	TGT	GAC	GAG	TGC	CAC	TCC	ACG	GAT	GCC	ACA	TCC	ATC	
CTG	TAT	TAT	TAA	ACA	CTG	CTC	ACG	GTG	AGG	TGC	CTA	CGG	TGT	AGG	TAG	

Figure 10 (continued)

**PCT/US91/02210**

480						485				490					
Val	Ser	Val	Ile	Pro	Thr	Ser	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp
GTG	TCC	GTC	ATC	CCG	ACC	AGC	GGC	GAT	GTT	GTC	GTC	GTG	GCA	ACC	GAT
CAC	AGG	CAG	TAG	GGC	TGG	TCG	CCG	CTA	CAA	CAG	CAG	CAC	CGT	TGG	CTA

**Figure 10 (continued)**